

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 1, 2003, 09:11:12 ; Search time 36 Seconds
(without alignments)
658.850 Million cell updates/sec

Title: US-09-965-528-16
Perfect score: 964
Sequence: 1 MAAARLCLLLLLSTCVALL.....FSEWGSPHAAVPRELSPLDL 178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :		A Geneseq 101002.*	
	1:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*	
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	9:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*	
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	14:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*	
	15:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*	
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	17:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*	
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	19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*	
	20:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*	
	21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*	
	22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*	
	23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	964	100.0	178	22 AAB48072	Human extracellular
2	378.5	39.3	95	20 AAY05276	Pancreatic polypep
3	186	19.3	36	19 AAW76722	Pancreatic polypep
4	186	19.3	36	21 AAB12179	Human pancreatic p
5	186	19.3	36	21 AAY87962	Human neuropeptide
6	186	19.3	36	21 AAY53658	Amino acid sequenc
7	186	19.3	36	22 AAB91217	Pancreatic polypep
8	186	19.3	36	22 AAU06196	Mammalian pancreat
9	177	18.4	36	21 AAY53657	Amino acid sequenc
10	139	14.4	36	21 AAB12180	Rat pancreatic pol

11	139	14.4	36	21 AAY87963	Rat neuropeptide p
12	139	14.4	36	22 AAB91221	Pancreatic polypep
13	114	11.8	36	22 AAB91220	Pancreatic polypep
14	110	11.4	36	11 AAR07276	Porcine small inte
15	110	11.4	36	22 AAB91226	Peptide YY SEQ ID
16	109	11.3	97	21 AAB08020	Amino acid sequenc
17	109	11.3	176	22 AAG75364	Human colon cancer
18	107	11.1	20	21 AAY53660	Amino acid sequenc
19	107	11.1	36	22 AAB91109	Parathyroid hormon
20	104	10.8	223	22 AAC06156	Human polypeptide
21	103.5	10.7	97	20 AAY43334	Neuropeptide Y. S
22	103.5	10.7	97	20 AAY23828	Human prepro-neuro
23	103.5	10.7	97	21 AAB35660	Human neuropeptide
24	103.5	10.7	97	21 AAY57078	Human neuropeptide
25	103.5	10.7	97	22 AAE07919	Human neuropeptide
26	103.5	10.7	97	22 AAE07955	Human neuropeptide
27	103.5	10.7	97	22 AAB85107	Human neuropeptide
28	103.5	10.7	97	22 AAB85118	Human neuropeptide
29	103.5	10.7	97	22 AAB80278	Human neuropeptide
30	103.5	10.7	97	23 AAC18305	Human prostate can
31	103.5	10.7	97	23 AAC18054	Human neuropeptide
32	102	10.6	216	21 AAY92665	MUC-1 analogue con
33	102	10.6	3014	22 AAU68533	Human novel cytoki
34	102	10.6	3014	22 AAU02196	Seven-pass transme
35	102	10.6	3028	22 AAE08586	Human NOV7 protein
36	100.5	10.4	505	18 AAW23275	Bordetella pertuss
37	100.5	10.4	532	22 ABG20464	Novel human diagno
38	99	10.3	36	11 AAR07277	Porcine small inte
39	99	10.3	36	15 AAR62050	Human peptide YY (
40	99	10.3	36	15 AAR62049	Porcine peptide YY
41	99	10.3	36	17 AAR97740	Porcine peptide YY
42	99	10.3	36	17 AAR97741	Human peptide YY.
43	99	10.3	36	18 AAW15365	[im-DNP-His26]-PYY
44	99	10.3	36	19 AAW51800	Porcine peptide YY
45	99	10.3	36	19 AAW51801	Human peptide YY.

ALIGNMENTS

RESULT 1	
ID	AAB48072
XX	AAB48072 standard; protein; 178 AA.
AC	AAB48072;
XX	19-MAR-2001 (first entry)
DT	Human extracellular signaling molecule (EXCS) (ID 5037143CD1).
DE	Extracellular signaling molecule; EXCS; anti-inflammatory; human;
XX	immunosuppressive; cytostatic; neuroprotective; gastrointestinal;
KW	viricide; antibacterial; anti-HIV; human immunodeficiency virus;
KW	antinfertility; cerebroprotective; nootropic; antiulcer; antifungal;
KW	anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;
KW	keratolytic; protozoacide; gene therapy.
OS	Homo sapiens.
XX	WO200070049-A2.
PN	23-NOV-2000.
XX	19-MAY-2000; 2000WO-US13975.
PF	19-MAY-1999; 99US-0134949.
XX	15-JUL-1999; 99US-0144270.
PR	30-JUL-1999; 99US-0146700.
PR	04-OCT-1999; 99US-0157508.
XX	(INCY-) INCYTE GENOMICS INC.
PA	Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;
XX	
PI	

RESULT 3

AAW76722
ID AAW76722 standard; peptide; 36 AA.

AC AAW76722;

XX 13-JAN-1999 (first entry)

XX Pancreatic polypeptide fragment for NIDDM treatment.

XX Non-insulin dependent diabetes mellitus; NIDDM; hepatic glucose;
KW pancreatic polypeptide; PP; treatment; Gs protein alpha subunit;
KW inhibitor; cyclic adenosine monophosphate; cAMP; glucagon; secretion;
KW exocrine pancreas; beta cell; pancreatic islet hypertrophy; insulin;
KW neurotrophin Y; hyperglycaemia.

XX Homo sapiens.

XX US5830434-A.

XX 03-NOV-1998.

XX 26-FEB-1997; 97US-0806203.

XX 26-FEB-1997; 97US-0806203.

XX (UYSC-) UNIV SOUTH CAROLINA MEDICAL RES FOUND.

XX Gettys T, Taylor IL;

XX WPI; 1998-609185/51.

XX Treatment of non-insulin-dependent diabetes mellitus - with
PT pancreatic polypeptide or C-terminal fragment

XX Disclosure; Column 3; 11pp; English.

XX This human pancreatic polypeptide fragment is used in a method for
treating non-insulin-dependent diabetes mellitus (NIDDM). The method
involves administering a composition comprising pancreatic polypeptide or
C-terminal pancreatic polypeptide fragment in a carrier. Screening a
composition for the ability to treat NIDDM is also possible and involves
determining if the composition decreases hepatic expression of the
alpha subunit of a Gs protein in a liver cell plasma membrane, thereby
inhibiting stimulation of cyclic adenosine monophosphate (cAMP) by
glucagon, determined if the composition binds the vagal nuclear complex
and inhibits secretions of digestive enzymes by the exocrine pancreas,
thereby inhibiting beta cell and pancreatic islet hypertrophy or
determining if the composition binds the arcuate nucleus in the
hypothalamus and potentiates the effect of leptin in reducing
neurotrophin Y synthesis, thereby enhancing insulin sensitivity and
reversing the effects of neurotrophin Y. The NIDDM treatment method
decreases hyperglycaemia and increases insulin sensitivity without
additional detrimental effects.

XX Sequence 36 AA;

Query Match 19.3%; Score 186; DB 19; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.5e-10;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64

Db 1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35

RESULT 4

AAB12179

ID AAB12179 standard; peptide; 36 AA.

XX AAB12179;

XX 20-JUN-2001 (first entry)
XX Human pancreatic polypeptide.
DE Human; neurotrophin Y; luteinizing hormone; reproductive system;
KW NPY; NPY-Y4 receptor; precocious puberty; pancreatic polypeptide;
KW polycystic ovary syndrome; endometriosis; benign prostatic hyperplasia;
KW delayed puberty; amenorrhea; breast cancer; prostate cancer; PP.

XX Homo sapiens.

XX Key Location/Qualifiers
FT Modified-site 36
FT /note= "C-terminal amide"

XX WO2000030674-A1.

XX 02-JUN-2000.

XX 26-NOV-1999; 99WO-GB03963.

XX 26-NOV-1998; 98GB-0025969.

XX 13-MAY-1999; 99GB-0011178.

XX (FERR) FERRING BV.

XX Broqua P, Akinsanya K, Hayward A;

XX WPI; 2000-399931/34.

XX Treating human reproductive disorders such as amenorrhea, delayed
PT puberty, polycystic ovary syndrome and endometriosis, comprises
PT administering a neurotrophin Y-Y4 receptor ligand -

XX Disclosure; Page 2; 17pp; English.

XX Neurotrophin Y (NPY) (AAB12177) has a number of effects on the
reproductive system. NPY is one of a family of neuropeptides. Other
members of the family include peptide YY (PYY), see AAB12177), and the
present sequence, human pancreatic polypeptide (HPP). Rat pancreatic
polypeptide is described in AAB12180. Selective NPY-Y4 receptor agonists
have been found (see AAB12181 to AAB12183). The NPY-Y4 receptor agonists
cause an increase in the circulating levels of luteinizing hormone (LH)
and hence improve the fertility of animals with compromised reproductive
function. The NPY-Y4 agonists may be used to treat human reproductive
disorders such as delayed puberty and amenorrhea. In addition, NPY-Y4
antagonists may be used to treat human reproductive disorders such as
precocious puberty, endometriosis, polycystic ovary syndrome, benign
prostatic hyperplasia and hormone-dependent neoplasias e.g. breast cancer
and prostate cancer. The present sequence was used in a sequence homology
comparison.

XX Sequence 36 AA;

Query Match 19.3%; Score 186; DB 21; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.5e-10;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64

Db 1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35

RESULT 5

AA87962

ID AA87962 standard; peptide; 36 AA.

XX AA87962;

XX 18-SEP-2000 (first entry)

XX Human neurotrophin PP fragment.

XX Neuropeptide; human; treatment; reproductive disorder; neuropeptide Y;
KW endocrine; gynecological; cytostatic; puberty; endometriosis;
KW polycystic ovary syndrome; prostatic hyperplasia; amenorrhea.
XX Homo sapiens.
OS GB2344050-A.
PN 31-MAY-2000.
PD 26-NOV-1998; 98GB-0025969.
PF 26-NOV-1998; 98GB-0025969.
PR (FERR) FERRING BV.
XX Akinsanya K, Hayward A, Broqua P;
PI WPI; 2000-331548/29.
DR Compositions containing a neuropeptide Y Y4 receptor ligand selective
for the hypothalamic-pituitary-gonadal axis, for treatment of
reproductive disorders e.g. delayed or precocious puberty,
endometriosis and benign prostatic hyperplasia -
XX Disclosure; Page 2; 12pp; English.
XX This invention describes the novel use of a composition containing a
neuropeptide Y (NPY) Y4 receptor ligand for treatment of human
reproductive disorders. The products described in the invention have
endocrine, gynecological and cytostatic activity and can be used for the
treatment of reduced reproductive function, delayed puberty, supranormal
function of the reproductive organs, precocious puberty, endometriosis,
polycystic ovary syndrome, benign prostatic hyperplasia, impaired
reproductive function or amenorrhea. This sequence represents the human
PP neuropeptide which is used in the method of the invention.
XX
SQ Sequence 36 AA;
Query Match 19.3%; Score 186; DB 21; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
Db 1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35
RESULT 6
AY53658
ID AAY53658 standard; protein; 36 AA.
XX
AC AAY53658;
XX
DT 22-FEB-2000 (first entry)
XX
DE Amino acid sequence of the human pancreatic polypeptide.
XX
KW Human; pancreatic polypeptide; transplanted pancreatic tissue viability;
KW graft damage; graft deterioration; immunosuppressive treatment; insulin;
KW pancreatic tissue; diabetic; clinical monitor;
KW early transplant viability; transplant survival.
XX
OS Homo sapiens.
XX WO9958979-A1.
PN 18-NOV-1999.
XX
PD 13-MAY-1999; 99WO-AU00361.
PF
XX 13-MAY-1998; 98AU-0003490.
PR

XX (SESY-) SOUTHEASTERN SYDNEY AREA HEALTH SERVICE.
PA (UNIX) UNISEARCH LTD.
XX Tutch BE, Amaratunga AP, Brown AS, Bucknall MP, Duncan MW;
XX WPI; 2000-053124/04.
XX
XX New method for monitoring transplanted pancreatic tissue viability in
mammal -
XX
XX Disclosure; Fig 7; 70pp; English.
XX
XX The present sequence represents a human pancreatic polypeptide. The
polypeptide is used in the method of the invention, for monitoring
transplanted pancreatic tissue viability. The method comprises screening
for the modulation of the level of a transplanted tissue derived molecule
or its derivative, e.g. pancreatic polypeptide, in the body fluid. The
method is useful for monitoring the viability of transplanted pancreatic
tissue in a mammal by screening for an increase or decrease in the level
of a transplanted tissue derived molecule. The method is an indicator of
graft damage or deterioration which would permit the commencement of
immunosuppressive treatment. The method is especially useful for
monitoring the viability of insulin producing foetal pancreatic tissue
which has been transplanted into diabetic patients. The method is also
useful as a non-invasive clinical monitor of early transplant viability
and on-going transplant survival.
XX
SQ Sequence 36 AA;
Query Match 19.3%; Score 186; DB 21; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
Db 1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35
RESULT 7
AAB91217
ID AAB91217 standard; Peptide; 36 AA.
XX
XX AAB91217;
AC
XX
DT 22-JUN-2001 (first entry)
XX
DE Pancreatic polypeptides (PP) peptide SEQ ID NO:391.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200069900-A2.
PN
XX
PD 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
PI WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT

PT peptidase degradation, useful for increasing length of in vivo activity

PT -

XX

PS Disclosure; Page 325; 733pp; English.

XX

CC The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.

CC

XX

SQ Sequence 36 AA;

Query Match 19.3%; Score 186; DB 22; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
|||||

Db 1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35

RESULT 8

AAU06196

ID AAU06196 standard; peptide; 36 AA.

XX

AC AAU06196;

XX

DT 04-DEC-2001 (first entry)

XX

DE Mammalian pancreatic polypeptide (PP).

XX

KW Mammalian; brain aluminium concentration; central nervous system;
CNS; peptide tyrosine-tyrosine receptor; PYY receptor; PP receptor;
pancreatic polypeptide receptor; Alzheimer's disease; neurotropic;
neuro protective.

OS Mammalia.

XX

PN WO200158409-A2.

XX

PD 16-AUG-2001.

XX

PF 07-FEB-2001; 2001WO-US03952.

XX

PR 08-FEB-2000; 2000US-0499980.

XX

PA (UYNC-) UNIV NORTH CAROLINA STATE.

XX

PI Croom WJ, Berg BM, Taylor IL;

XX

DR WPI; 2001-550001/61.

XX

PT Reducing aluminium levels in the central nervous system, for the treatment of Alzheimer's disease comprises administration of a peptide tyrosine receptor agonist or a pancreatic polypeptide receptor agonist

XX

PS Disclosure; Page 6; 52pp; English.

XX

CC The present invention relates to a method of reducing aluminium levels

CC in the central nervous system (CNS). The method comprises administration of a peptide tyrosine-tyrosine (PYY) receptor agonist or a pancreatic polypeptide (PP) receptor agonist. The method is useful for the treatment of Alzheimer's disease and for reducing aluminium levels in the central nervous system, especially the brain, of a subject. The treatments are effective and do not impart excessive toxicological effects. The present sequence represents mammalian pancreatic PP.

XX

SQ Sequence 36 AA;

Query Match 19.3%; Score 186; DB 22; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
|||||

Db 1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35

RESULT 9

AAU53657

ID AAU53657 standard; protein; 36 AA.

XX

AC AAU53657;

XX

DT 22-FEB-2000 (first entry)

XX

DE Amino acid sequence of the porcine pancreatic polypeptide.

XX

KW Pig; pancreatic polypeptide; transplanted pancreatic tissue viability;
graft damage; graft deterioration; immunosuppressive treatment; insulin;
pancreatic tissue; diabetic; clinical monitor;
early transplant viability; transplant survival.

OS Sus sp.

XX

PN WO9958979-A1.

XX

PD 18-NOV-1999.

XX

PF 13-MAY-1999; 99WO-AU00361.

XX

PR 13-MAY-1998; 98AU-0003490.

XX

PA (SES-) SOUTHEASTERN SYDNEY AREA HEALTH SERVICE.
(UNIX) UNISEARCH LTD.

XX

PI Tuch BE, Amaratunga AP, Brown AS, Bucknall MP, Duncan MW;

XX

DR WPI; 2000-053124/04.

XX

PT New method for monitoring transplanted pancreatic tissue viability in mammal

PT

PS Disclosure; Fig 7; 70pp; English.

XX

CC The present sequence represents a porcine pancreatic polypeptide. The polypeptide is used in the method of the invention, for monitoring transplanted pancreatic tissue viability. The method comprises screening for the modulation of the level of a transplanted tissue derived molecule or its derivative, e.g. pancreatic polypeptide, in the body fluid. The method is useful for monitoring the viability of transplanted pancreatic tissue in a mammal by screening for an increase or decrease in the level of a transplanted tissue derived molecule. The method is an indicator of graft damage or deterioration which would permit the commencement of immunosuppressive treatment. The method is especially useful for monitoring the viability of insulin producing foetal pancreatic tissue which has been transplanted into diabetic patients. The method is also useful as a non-invasive clinical monitor of early transplant viability and on-going transplant survival.

CC

XX

SQ Sequence 36 AA;

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
DR WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
PS Disclosure; Page 327; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 36 AA;
Query Match 14.4%; Score 139; DB 22; Length 36;
Best Local Similarity 77.1%; Pred. No. 4.2e-06;
Matches 27; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
DB 1 APLEPMYPGDYATHEQRAQYETQLRRYINTLTRPR 35
RESULT 13
AAB91220
ID AAB91220 standard; Peptide; 36 AA.
XX
AC AAB91220;
XX
DT 22-JUN-2001 (first entry)
XX
DE Pancreatic polypeptides (PP) peptide SEQ ID NO:394.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.

OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
PI WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
PS Disclosure; Page 326; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 36 AA;
Query Match 11.8%; Score 114; DB 22; Length 36;
Best Local Similarity 60.0%; Pred. No. 0.00096;
Matches 21; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
DB 1 APSEPHHPGDQATQDLAQYSDLYQYITFFVTRPR 35
RESULT 14
AAR07276
ID AAR07276 standard; protein; 36 AA.
XX
AC AAR07276;
XX
DT 01-FEB-1991 (first entry)
XX
DE Porcine small intestine YY peptide analogue #1.
XX
KW porcine small intestine YY peptide; nerve-tropic activity.
XX
OS Synthetic.
XX
PN JP02225497-A.
XX
PD 07-SEP-1990.
XX
PF 27-FEB-1989; 89JP-0046089.
XX

PR 27-FEB-1989; 89JP-0046089.
XX (SUNR) SUNTORY LTD.
PA
XX WPI; 1990-316711/42.
DR
XX N-terminal analogue peptide(s) of porcine upper small intestine -
PT having improved central and peripheral nerve-tropic actions
PT
XX Claim 4; Page 1; 15pp; Japanese.
PS
XX The synthetic analogue is derived from porcine peptide YY. It has N-
CC terminal substitutions which render the core structure more stable.
CC The analogue also has improved internal-secretion inducing and nerve-
CC tropic activities. These include bradycardia, vasoconstriction and
CC acceleration of feeding behaviour. The analogue also inhibits smooth
CC muscle contraction in the ductus deferens and the uterus caused by
CC electrical stimuli. See also AAR07277 and AAR07278.
XX
SQ Sequence 36 AA;
Query Match 11.4%; Score 110; DB 11; Length 36;
Best Local Similarity 50.0%; Pred. No. 0.0023;
Matches 17; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
QY 31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
| : | | | | : | | : | | | | : | | : | | | |
Db 2 PSQPTYGEDASPEELSRYYASLRHYLNLVTRQR 35
RESULT 15
AAB91226
ID AAB91226 standard; Peptide; 36 AA.
XX
AC AAB91226;
XX
DT 22-JUN-2001 (first entry)
XX
DE Peptide YY SEQ ID NO:400.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
D 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
PS Disclosure; Page 329; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 36 AA;
Query Match 11.4%; Score 110; DB 22; Length 36;
Best Local Similarity 52.9%; Pred. No. 0.0023;
Matches 18; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY 31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
| : | | | | : | | : | | | | : | | : | | | |
Db 2 PIKPEAPGEDASPEELNRYRYASLRHYLNLTRPR 35
Search completed: March 1, 2003, 09:12:41
Job time : 38 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 1, 2003, 09:12:46 ; Search time 14 Seconds
(without alignments)
479.606 Million cell updates/sec

Title: US-09-965-528-16
Perfect score: 964
Sequence: 1 MAAARLCLSLLLSTCVALL.....FSEWGSPHAAVPRELPLDL 178

Scoring table: BLOSUM62
Gapop 10.0 , Gapekt 0.5

Searched: 174566 seqs, 37721826 residues 174566
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	964	100.0	178	9	US-09-965-528-16
2	378.5	39.3	95	10	US-09-757-712-2
3	186	19.3	36	12	US-10-016-969-1
4	103.5	10.7	97	9	US-10-002-048A-2
5	102	10.6	3014	10	US-09-737-149-2
6	99	10.3	36	12	US-10-016-969-2
7	99	10.3	36	12	US-10-038-045-4
8	96	10.0	36	12	US-10-038-045-2
9	94	9.8	36	12	US-10-038-045-1
10	93.5	9.7	508	9	US-10-057-136-20
11	93	9.6	410	9	US-10-078-650-14
12	92.5	9.6	1255	9	US-09-996-069-10
13	92	9.5	34	12	US-10-016-969-3
14	89	9.2	36	12	US-10-016-969-4
15	89	9.2	36	12	US-10-038-045-3
16	88	9.1	666	10	US-09-791-171-70
17	86	8.9	36	12	US-10-038-045-5
18	84.5	8.8	145	9	US-09-950-933A-45
19	84	8.7	34	12	US-10-016-969-5

20	84	8.7	1084	12	US-10-071-900-3	Sequence 3, Appli
21	83	8.6	1036	12	US-10-014-882-2	Sequence 2, Appli
22	81.5	8.5	365	10	US-09-876-187-4	Sequence 4, Appli
23	81.5	8.5	365	10	US-09-749-728B-15	Sequence 15, Appli
24	81	8.4	628	10	US-09-862-027-48	Sequence 48, Appli
25	81	8.4	726	10	US-09-770-689A-4	Sequence 4, Appli
26	81	8.4	803	10	US-09-770-689A-2	Sequence 2, Appli
27	81	8.4	5179	9	US-10-025-380-1068	Sequence 1068, Ap
28	81	8.4	5179	10	US-09-922-217-1068	Sequence 1068, Ap
29	81	8.4	5179	10	US-09-833-263-1068	Sequence 1068, Ap
30	80.5	8.4	100	9	US-09-965-131-6	Sequence 6, Appli
31	80	8.3	619	9	US-09-882-774-1	Sequence 1, Appli
32	79	8.2	207	10	US-09-349-954A-4	Sequence 4, Appli
33	79	8.2	207	10	US-09-912-436-4	Sequence 4, Appli
34	79	8.2	207	10	US-09-907-007-4	Sequence 4, Appli
35	78.5	8.1	163	9	US-09-854-133-41	Sequence 41, Appli
36	78.5	8.1	163	10	US-09-738-973-41	Sequence 41, Appli
37	78.5	8.1	755	10	US-09-919-497-57	Sequence 57, Appli
38	78.5	8.1	785	9	US-09-989-920-218	Sequence 218, App
39	78.5	8.1	891	9	US-09-976-059-18	Sequence 18, Appli
40	77.5	8.0	207	10	US-09-800-729-113	Sequence 113, App
41	77.5	8.0	208	10	US-09-800-729-151	Sequence 151, App
42	77.5	8.0	626	10	US-09-862-027-43	Sequence 43, Appli
43	77.5	8.0	635	9	US-09-738-626-6614	Sequence 6614, Ap
44	77.5	8.0	881	10	US-09-816-860A-2	Sequence 2, Appli
45	77	8.0	188	9	US-09-852-209A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-965-528-16
; Sequence 16, Application US/09965528
; Publication No. US20020187523A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: PF-0701 USA
; CURRENT APPLICATION NUMBER: US/09/965,528
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/134,949
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/144,270
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/146,700
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/157,508
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 16
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020187523A1 5037143CD1
US-09-965-528-16

Query Match 100.0%; Score 964; DB 9; Length 178;
Best Local Similarity 100.0%; Pred. No. 2.9e-72;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAAARCLSLLLSTCVALLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
Db 1 MAAARCLSLLLSTCVALLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
QY 61 TRPRCVPQLGREIPAPGTLGPHIPGHTLSAPAPAPSRPALGKTGHLCTGLDQCALGK 120
Db 61 TRPRCVPQLGREIPAPGTLGPHIPGHTLSAPAPAPSRPALGKTGHLCTGLDQCALGK 120
QY 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPRELSPLDL 178
Db 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPRELSPLDL 178

RESULT 2
US-09-757-712-2
; Sequence 2, Application US/09757712
; Patent No. US20010016339A1
; GENERAL INFORMATION:
; APPLICANT: SOUTHAN, CHRISTOPHER
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30015-C1
; CURRENT APPLICATION NUMBER: US/09/757,712
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: EP 97307187.1
; PRIOR FILING DATE: 1997-09-16
; PRIOR APPLICATION NUMBER: 09/110,715
; PRIOR FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 95
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-757-712-2

Query Match 39.3%; Score 378.5; DB 10; Length 95;
Best Local Similarity 47.2%; Pred. No. 1.5e-24;
Matches 84; Conservative 4; Mismatches 7; Indels 83; Gaps 1;

QY 1 MAAARCLSLLLSTCVALLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
Db 1 MAAARCLSLLLSTCVALLQPLLGAQGAPLEPLYPGDNTTPEQMAQYTAELRRYINML 60
QY 61 TRPRCVPQLGREIPAPGTLGPHIPGHTLSAPAPAPSRPALGKTGHLCTGLDQCALGK 120
Db 61 TR-----62
QY 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPRELSPLDL 178
Db 63 -----HRYGERDKEDTLAFSEWGSSHAAVPRELSPLDL 95

RESULT 3
US-10-016-969-1
; Sequence 1, Application US/10016969
; Patent No. US20020141985A1
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Pittner, Richard
; APPLICANT: Young, Andrew
; APPLICANT: Paterniti, James
; TITLE OF INVENTION: Peptide YY and Peptide YY Agonists for the Treatment of Metabolic
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 24001-010
; CURRENT APPLICATION NUMBER: US/10/016,969
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/256,216
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-016-969-1

Query Match 19.3%; Score 186; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
Db 1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35

RESULT 4
US-10-002-048A-2
; Sequence 2, Application US/10002048A
; Publication No. US20020182616A1
; GENERAL INFORMATION:
; APPLICANT: Wahlestedt, Claes
; APPLICANT: Ding, Bo
; TITLE OF INVENTION: Single Nucleotide Polymorphisms
; FILE REFERENCE: 10806-143
; CURRENT APPLICATION NUMBER: US/10/002,048A
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: SE 0004035-2
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 97
; TYPE: PRT
; ORGANISM: human
US-10-002-048A-2

Query Match 10.7%; Score 103.5; DB 9; Length 97;
Best Local Similarity 39.1%; Pred. No. 0.056;
Matches 25; Conservative 12; Mismatches 18; Indels 9; Gaps 2;

QY 1 MAAARCLSLLLSTCVALLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
Db 9 LSGLTLALSLLV---CLGAL-----AEAYPSKPDNPGEDAPAEEDMARYYSALRHYINLI 59
QY 61 TRPR 64
Db 60 TRQR 63

RESULT 5
US-09-737-149-2
; Sequence 2, Application US/09737149
; Patent No. US20020077466A1
; GENERAL INFORMATION:
; APPLICANT: Spaderna, Steven K
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Muralidhara, Padigaru
; APPLICANT: Spytek, Kimberly A.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-620 CIP
; CURRENT APPLICATION NUMBER: US/09/737,149
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/170,564
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: 60/173,165
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: 60/173,362
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: 60/173,544
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 60/174,404
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 60/174,962
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 60/223,929
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```

; GENERAL INFORMATION:
; APPLICANT: Fujimoto, Katsumi
; APPLICANT: Shin, Mei
; APPLICANT: Kato, Yukio
; TITLE OF INVENTION: NOVEL bHLH TYPE TRANSCRIPTION FACTOR
; TITLE OF INVENTION: GENES DEC2
; FILE REFERENCE: 06501-101001
; CURRENT APPLICATION NUMBER: US/10/078,650
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/JP00/03991
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: JP 11-233286
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Mus musculus
; -10-078-650-14

Query Match          9.6%; Score 93; DB 9; Length 410;
Best Local Similarity 29.9%; Pred. No. 2.1;
Matches 38; Conservative 6; Mismatches 53; Indels 30; Gaps 4;

QY  2  AARUCLSLLSTCVALLQLLGAQG-----APLEVPYPGDNATPEQMAQYAA 51
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  286 AAAPFCLFFYLLSPSAAYVQWLDKSLDKYLYPAAAPFFLLYPGIPAAAAAA--AA 343

QY  52  DLRRYINMLTRP-----RCVPQLGREIPAPGTLGPLHHPGHTLSP-----AP 93
      :||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  344 AFPCLSSVLSPPPEKAGATAGAPFLAHEVAPPGPLRPQHAHSRTHLPRAVNPSSQEDAT 403

QY  94  APAPSRP 100
      ||| |||
Db  404 QPAKDAP 410

RESULT 12
US-09-996-069-10
; Sequence 10, Application US/09996069
; Publication No. US20030036199A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; APPLICANT: Bamdad, R. Shoshana
; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBITORS
; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER
; FILE REFERENCE: M01015/70071
; CURRENT APPLICATION NUMBER: US/09/996,069
; CURRENT FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-069-10

Query Match          9.6%; Score 92.5; DB 9; Length 1255;
Best Local Similarity 27.1%; Pred. No. 8.3;
Matches 42; Conservative 8; Mismatches 60; Indels 45; Gaps 7;

QY  23  PLLGAQGAPLEVPYPGDNATPEQMAQYAADLRRYINMLTRPRCVPLGREIPAPGTLGPL 82
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  734 PAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTR-----PAPGSTAP- 773

QY  83  HIPGHTLSAP--APAP-----SRPALGKT---GHLCSSTGLD-QCALGKM 121
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  774 --PAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGST 831

QY  122 VPTGRYETGGLAPGHSACPCCLFPBRYGKRHKEDT 156
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  832 APPAHGVTS--APDTRPAPGSTAPPAHGVTSAPDT 864
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```

RESULT 13
US-10-016-969-3
; Sequence 3, Application US/10016969
; Patent No. US20020141985A1
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Pittner, Richard
; APPLICANT: Young, Andrew
; APPLICANT: Paterniti, James
; TITLE OF INVENTION: Peptide YY and Peptide YY Agonists for the Treatment of Metabolic Disorders
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 24001-010
; CURRENT APPLICATION NUMBER: US/10/016,969
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/256,216
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-969-3

Query Match          9.5%; Score 92; DB 12; Length 34;
Best Local Similarity 45.5%; Pred. No. 0.15;
Matches 15; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY  32  LEVPYPGDNATPEQMAQYAADLRRYINMLTRPR 64
      :|| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  1  IKPEAPGEDASPEELNRYAYASLRHYLNLTQR 33
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RESULT 14
US-10-016-969-4
; Sequence 4, Application US/10016969
; Patent No. US20020141985A1
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Pittner, Richard
; APPLICANT: Young, Andrew
; APPLICANT: Paterniti, James
; TITLE OF INVENTION: Peptide YY and Peptide YY Agonists for the Treatment of Metabolic Disorders
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 24001-010
; CURRENT APPLICATION NUMBER: US/10/016,969
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/256,216
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-969-4

Query Match          9.2%; Score 89; DB 12; Length 36;
Best Local Similarity 50.0%; Pred. No. 0.28;
Matches 17; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY  31  PLEVPYPGDNATPEQMAQYAADLRRYINMLTRPR 64
      |:|| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  2  PSKPDNPGEDAPADMARYYSALRHYINLTQR 35
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```

RESULT 15
US-10-038-045-3
; Sequence 3, Application US/10038045
; Patent No. US20020150964A1
; GENERAL INFORMATION:
```

```
;;
;; APPLICANT: Mor, Amram
;; Vouldoukis, Ioannis
;; Nicolas, Pierre
;; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
;; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
;;
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds LLP
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10036-2811
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows
;; SOFTWARE: FastSEQ for Windows Version 2.0b
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/038,045
;; FILING DATE: 02-Jan-2002
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/181,941
;; FILING DATE: 28-Oct-1998
;; APPLICATION NUMBER: US 08/574,701
;; FILING DATE: 19-DEC-1995
;; APPLICATION NUMBER: FR 95 07831
;; FILING DATE: 29-JUN-1995
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 3909-0021-999
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-493-4935
;; TELEFAX: 650-493-5556
;; TELEX: 66141 PENNIE
;;
;; INFORMATION FOR SEQ ID NO: 3:
;;
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 36 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; MOLECULE TYPE: NO. US20020150964A1e
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-038-045-3

Query Match 9.2%; Score 89; DB 12; Length 36;
Best Local Similarity 50.0%; Pred. No. 0.28;
Matches 17; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
| : | | : | | : | | : | | : | | : | |
Db 2 PSKPDNPGEDAPAEDMAKYYSALRHYINLITRQR 35

Search completed: March 1, 2003, 09:17:19
Job time : 16 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 1, 2003, 09:11:46 ; Search time 143 Seconds
(without alignments)
802.535 Million cell updates/sec

Title: US-09-965-528-16
Perfect score: 964
Sequence: 1 MAAARLCLSLLLSTCVALL.....FSEWGSPHAAVPRELSPDL 178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues 4569144
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US080_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
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7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
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11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep.*
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16: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/1/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/1/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/1/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/1/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US099_COMB.pep.*
24: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
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26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	964	100.0	178	23 US-09-965-528-16	Sequence 16, Appl
2	964	100.0	178	23 US-09-979-300-16	Sequence 16, Appl
3	964	100.0	178	27 US-60-144-270-6	Sequence 6, Appli
4	441.5	45.8	95	25 US-10-177-488-86	Sequence 86, Appl
5	379	39.3	87	27 US-60-200-109-982	Sequence 982, App
6	378.5	39.3	95	15 US-09-110-715-2	Sequence 2, Appli

7	378.5	39.3	95	21	US-09-757-712-2	Sequence 2, Appli
8	378.5	39.3	95	24	US-10-036-657-32	Sequence 32, Appl
9	356	36.9	94	27	US-60-200-109-981	Sequence 981, App
10	311	32.3	64	27	US-60-196-718-4967	Sequence 4967, Ap
11	310.5	32.2	92	27	US-60-192-739-3324	Sequence 3324, Ap
12	310.5	32.2	92	27	US-60-194-243-2397	Sequence 2397, Ap
13	186	19.3	36	1	PCT-US02-30533-25	Sequence 25, Appl
14	186	19.3	36	20	US-09-657-276-391	Sequence 391, App
15	186	19.3	36	24	US-10-016-969-1	Sequence 1, Appli
16	186	19.3	38	1	PCT-US02-22821-112	Sequence 112, App
17	186	19.3	38	25	US-10-197-954-112	Sequence 112, App
18	182	18.9	36	1	PCT-US02-30533-28	Sequence 28, Appl
19	182	18.9	36	27	US-60-196-718-4968	Sequence 4968, Ap
20	177	18.4	36	1	PCT-US02-30533-26	Sequence 26, Appl
21	177	18.4	36	1	PCT-US02-30533-27	Sequence 27, Appl
22	176	18.3	36	1	PCT-US02-30533-29	Sequence 29, Appl
23	174	18.0	33	27	US-60-195-053-1911	Sequence 1911, Ap
24	169.5	17.6	37	1	PCT-US02-30533-32	Sequence 32, Appl
25	168	17.4	36	1	PCT-US02-30533-3	Sequence 3, Appli
26	162	16.8	32	27	US-60-195-053-1467	Sequence 1467, Ap
27	154	16.0	36	1	PCT-US02-30533-31	Sequence 31, Appl
28	139	14.4	36	1	PCT-US02-30533-30	Sequence 30, Appl
29	139	14.4	36	20	US-09-657-276-395	Sequence 395, App
30	123	12.8	36	1	PCT-US02-30533-35	Sequence 35, Appl
31	114	11.8	36	20	US-09-657-276-394	Sequence 394, App
32	113	11.7	36	1	PCT-US02-30533-11	Sequence 11, Appl
33	110	11.4	36	20	US-09-657-276-400	Sequence 400, App
34	109	11.3	97	18	US-09-499-526-3	Sequence 3, Appli
35	109	11.3	176	1	PCT-US00-26524B-6128	Sequence 6128, Ap
36	109	11.3	176	25	US-10-106-698-6138	Sequence 6138, Ap
37	107	11.1	36	20	US-09-657-276-283	Sequence 283, App
38	106	11.0	36	1	PCT-US02-30533-34	Sequence 34, Appl
39	103.5	10.7	97	1	PCT-US00-19666-65	Sequence 65, Appl
40	103.5	10.7	97	1	PCT-US00-34758-3	Sequence 3, Appli
41	103.5	10.7	97	1	PCT-US02-23913-289	Sequence 289, App
42	103.5	10.7	97	13	US-08-994-946-6	Sequence 6, Appli
43	103.5	10.7	97	17	US-09-310-707A-16	Sequence 16, Appl
44	103.5	10.7	97	21	US-09-708-344-7	Sequence 7, Appli
45	103.5	10.7	97	21	US-09-708-344A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-965-528-16
; Sequence 16, Application US/09965528
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: PF-0701 USA
; CURRENT APPLICATION NUMBER: US/09/965,528
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/134,949
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/144,270
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/146,700
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/157,508
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 16


```

; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 86
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-177-488-86

Query Match          45.8%; Score 441.5; DB 25; Length 95;
Best Local Similarity 53.4%; Pred. No. 3.2e-29;
Matches 95; Conservative 0; Mismatches 0; Indels 83; Gaps 1;

QY 1 MAAARCLSLLLSTCVALLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
   |||||
Db 1 MAAARCLSLLLSTCVALLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60

QY 61 TRPRCVPQLGREIPAPGTLGPHLPGHTLSAPAPAPSRPALGKTGHLCTGLDQCALGK 120
   ||
Db 61 TR----- 62

121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPPHAAVPRELSPLDL 178
   |||||
Db 63 -----PRYGKRHKEDTLAFSEWGSPPHAAVPRELSPLDL 95

RESULT 5
US-60-200-109-982
; Sequence 982, Application US/60200109
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000484
; CURRENT APPLICATION NUMBER: US/60/200,109
; CURRENT FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 1348
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 982
; LENGTH: 87
; TYPE: PRT
; ORGANISM: HUMAN
US-60-200-109-982

Query Match          39.3%; Score 379; DB 27; Length 87;
Best Local Similarity 50.3%; Pred. No. 5.5e-24;
Matches 86; Conservative 0; Mismatches 1; Indels 84; Gaps 2;

1 MAAARCLSLLLSTCVALLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
   |||||
1 MAAARCLSLLLSTCVALLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60

QY 61 TRPRCVPQLGREIPAPGTLGPHLPGHTLSAPAPAPSRPALGKTGHLCTGLDQCALGK 120
   ||
Db 61 TR----- 62

121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPPHAAVPRELSPLDL 171
   |||||
Db 63 -----PRYGKRHKEDTLAFS-GGSPHAAVPR 87

RESULT 6
US-09-110-715-2
; Sequence 2, Application US/09110715
; GENERAL INFORMATION:
; APPLICANT: SOUTHAN, CHRISTOPHER
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
```

```

; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/110,715
; FILING DATE: 07-JULY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 97307187.1
; FILING DATE: 16-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-30015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-110-715-2

Query Match          39.3%; Score 378.5; DB 15; Length 95;
Best Local Similarity 47.2%; Pred. No. 6.7e-24;
Matches 84; Conservative 4; Mismatches 7; Indels 83; Gaps 1;

QY 1 MAAARCLSLLLSTCVALLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
   |||||
Db 1 MAAACRCLSLLLSTCVALLQPLLGAQGAPLEPLYPGDNATPEQMAQYTAELRRYINML 60

QY 61 TRPRCVPQLGREIPAPGTLGPHLPGHTLSAPAPAPSRPALGKTGHLCTGLDQCALGK 120
   ||
Db 61 TR----- 62

121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPPHAAVPRELSPLDL 178
   |||||
Db 63 -----HRYGERDKEDTLAFSEWGSPPHAAVPRELSPLDL 95

RESULT 7
US-09-757-712-2
; Sequence 2, Application US/09757712
; GENERAL INFORMATION:
; APPLICANT: SOUTHAN, CHRISTOPHER
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30015-C1
; CURRENT APPLICATION NUMBER: US/09/757,712
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: EP 97307187.1
; PRIOR FILING DATE: 1997-09-16
; PRIOR APPLICATION NUMBER: 09/110,715
; PRIOR FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 95
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-757-712-2

Query Match          39.3%; Score 378.5; DB 21; Length 95;
Best Local Similarity 47.2%; Pred. No. 6.7e-24;
Matches 84; Conservative 4; Mismatches 7; Indels 83; Gaps 1;

QY 1 MAAARCLSLLLSTCVALLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
```

```

Db      1  MAAACRCLSLLLLSTCVALLLQPLLGGARGAPLEPLYPGDNTTPEQMAQYTAELRRYINML 60
QY      61  TRPRCVQLGREIPAPGTLGPLHIPGHTLSPAPAPAPSRPALGKTGHLCSGLDQCALGK 120
Db      61  TR----- 62
QY      121 MVPTGRYETGGLAPGHSACPCCLFPPTYCKRKHKEDTLAFSEWGSPHAAVPRELSPDL 178
Db      63  -----HRYGERDKEDTLAFSEWGSSHAAVPRELSPDL 95

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```

RESULT 8
US-10-036-657-32
; Sequence 32, Application US/10036657
; GENERAL INFORMATION:
; APPLICANT: Earl Francis Albone, et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: GP-70778B-C1
; CURRENT APPLICATION NUMBER: US/10/036,657
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 95
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-036-657-32

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Query Match	39.3%;	Score 378.5;	DB 24;	Length 95;
Best Local Similarity	47.2%;	Pred. No. 6.7e-24;		
Matches 84;	Conservative	4;	Mismatches 7;	Indels 83;
				Gaps 1;

QY	1	MAAARCLSLLLSTCVALLQLPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYYINML	60
Dd	1	MAAACRCLSLLLSTCVALLQLPLLGARGAPLEPLYPGDNTTPEQMAQYTAEALRRYYINML	60
QY	61	TRPRCVPQLGREIPAPGTLGPLHPGHTLSAPAPAPSRPALGKTGHLCSTGLDQCALGK	120
Dd	61	TR-----TR-----	62

Qy	121	MVPTGRYTGGLAPGHSACPCCLFPFRYGKRRKHEDTLAFSEWGSPHAAVPRELSPIDL	178
Db	63	-----HRYGERDKEDTLAFSEWGSSHAAVPRELSPIDL	95

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RESULT 9
US-60-200-109-981
Sequence 981, Application US/60200109
GENERAL INFORMATION:
, APPLICANT: Beasley, Ellen
, TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
, TITLE OF INVENTION: USES THEREOF
, FILE REFERENCE: CL000484
, CURRENT APPLICATION NUMBER: US/60/200,109
, CURRENT FILING DATE: 2000-04-27
, NUMBER OF SEQ ID NOS: 1348
, SOFTWARE: FastSEQ for Windows Version 4.0
, SEQ ID NO 981
, LENGTH: 94
, TYPE: PRT
, ORGANISM: HUMAN
US-60-200-109-981

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Query Match 36.9%; Score 356; DB 27; Length 94;
Best Local Similarity 46.6%; Pred. No. 5.2e-22;
Matches 82; Conservative 2; Mismatches 8; Indels 84; Gaps 2;

Qy 1 MAAARCLSLLLSTCVALLQLPLGAAQGAFLPVYPGDNATPEQMAQYAADLRRYINWL 60

Dd 1 MAAARCLSLLLSTCVALLQLPLGAAQGAFLPVYPGDNATPEQMAQYAADLRRYINWL 60

```

QY 61 TRPRCVQLGREIPAPGTLGPLHIPGHTLSPAPAPAPSRPALGKTGHLCTGLDQCALGK 120
    ||
Db 61 TR----- 62

QY 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPhAAVPR-ELSP 175
    |||||
Db 63 -----PRYGKRHKEDTLAFSGGGVPACCCPQVSLTP 93

RESULT 10
US-60-196-718-4967
; Sequence 4967, Application US/60196718
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000456
; CURRENT APPLICATION NUMBER: US/60/196,718
; CURRENT FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4967
; LENGTH: 64
; TYPE: PRT
; ORGANISM: HUMAN
US-60-196-718-4967

```

Query Match 32.3%; Score 311; DB 27; Length 64;
Best Local Similarity 96.9%; Pred. No. 2.1e-18;
Matches 62; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MAAARCLCSLLLLSTCVALLLOPLLGAQGAPLEPVYPGDNATPEOMAQAADLRRYYINML
Dd	1	MAAARCLCSLLLLSTCVALLLOPLLGAQGAPLEPVYPGDNATPEOMAQAAGLRRYYINMQ
QY	61	TRPR 64
Dd	61	TRPR 64

```

RESULT 11
US-60-192-739-3324
; Sequence 3324, Application US/60192739
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000406
; CURRENT APPLICATION NUMBER: US/60/192,739
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 4532
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3324
; LENGTH: 92
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(92)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-192-739-3324

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Query Match	32.2%;	Score 310.5;	DB 27;	Length 92;
Best Local Similarity	40.6%;	Pred. No. 3.5e-18;		
Matches 71; Conservative	5;	Mismatches 16;	Indels 83;	Gaps 1;

[illegible]

Query Match 19.3%; Score 186; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
Db 1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35

RESULT 14
US-09-657-276-391
; Sequence 391, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 391
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-391

Query Match 19.3%; Score 186; DB 20; Length 36;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
Db 1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35

RESULT 15
US-10-016-969-1
; Sequence 1, Application US/10016969
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Pittner, Richard
; APPLICANT: Young, Andrew
; APPLICANT: Paterniti, James
; TITLE OF INVENTION: Peptide YY and Peptide YY Agonists for the Treatment of Metabolic
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 24001-010
; CURRENT APPLICATION NUMBER: US/10/016,969
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/256,216
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-969-1

Db 61 K----- 61

QY 122 VPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSHPAAVPRELSP 176
Db 62 -----PMYGERDKEDTLAFSEWGLPMLPPGEFDSL 92

RESULT 12
US-60-194-243-2397
; Sequence 2397, Application US/60194243
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000417
; CURRENT APPLICATION NUMBER: US/60/194,243
; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2397
; LENGTH: 92
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(92)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-194-243-2397

Query Match 32.2%; Score 310.5; DB 27; Length 92;
Best Local Similarity 40.6%; Pred. No. 3.5e-18;
Matches 71; Conservative 5; Mismatches 16; Indels 83; Gaps 1;

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QY 62 RPRCVPQLGREIPAPGTGLPLHPGHTLSPAPAPSRPALGKTGHLCTGLDQCALGKM 121
Db 61 K----- 61

QY 122 VPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSHPAAVPRELSP 176
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RESULT 13
PCT-US02-30533-25
; Sequence 25, Application PC/TUS0230533
; GENERAL INFORMATION:
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Bulter, Andrew
; TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Screen for Agents
; TITLE OF INVENTION: Modify Feeding Behavior
; FILE REFERENCE: 0899-63986
; CURRENT APPLICATION NUMBER: PCT/US02/30533
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Ovis aries
PCT-US02-30533-25

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 1, 2003, 09:12:05 ; Search time 25 Seconds
(without alignments)
663.560 Million cell updates/sec

Title: US-09-965-528-16
 Perfect score: 964
 Sequence: 1 MAAARLCLSLLLSTCVALL.....FSEWGSPHAAVPRELSPLDL 178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 494224 seqs, 93196565 residues

total number of hits satisfying chosen parameters: 4942224

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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7: /cgn2_6/ptodata/2/paa/us60_new_comb_pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match					
1	186	19.3	36	1	PCT-US02-31944A-25		Sequence 25, Appl
2	186	19.3	36	1	PCT-US02-30533A-25		Sequence 25, Appl
3	182	18.9	36	1	PCT-US02-31944A-28		Sequence 28, Appl
4	182	18.9	36	1	PCT-US02-30533A-28		Sequence 28, Appl
5	177	18.4	36	1	PCT-US02-31944A-26		Sequence 26, Appl
6	177	18.4	36	1	PCT-US02-31944A-27		Sequence 27, Appl
7	177	18.4	36	1	PCT-US02-30533A-26		Sequence 26, Appl
8	177	18.4	36	1	PCT-US02-30533A-27		Sequence 27, Appl
9	176	18.3	36	1	PCT-US02-31944A-29		Sequence 29, Appl
10	176	18.3	36	1	PCT-US02-30533A-29		Sequence 29, Appl
11	169.5	17.6	37	1	PCT-US02-31944A-32		Sequence 32, Appl
12	169.5	17.6	37	1	PCT-US02-30533A-32		Sequence 32, Appl
13	168	17.4	36	1	PCT-US02-31944A-3		Sequence 3, Appli
14	168	17.4	36	1	PCT-US02-30533A-3		Sequence 3, Appli
15	154	16.0	36	1	PCT-US02-31944A-31		Sequence 31, Appl
16	154	16.0	36	1	PCT-US02-30533A-31		Sequence 31, Appl
17	139	14.4	36	1	PCT-US02-31944A-30		Sequence 30, Appl
18	139	14.4	36	1	PCT-US02-30533A-30		Sequence 30, Appl
19	123	12.8	36	1	PCT-US02-31944A-35		Sequence 35, Appl
20	123	12.8	36	1	PCT-US02-30533A-35		Sequence 35, Appl
21	122	12.7	36	6	US-10-072-012-875		Sequence 875, App
22	116	12.0	98	6	US-10-072-012-710		Sequence 710, App
23	113	11.7	36	1	PCT-US02-31944A-11		Sequence 11, Appl
24	113	11.7	36	1	PCT-US02-30533A-11		Sequence 11, Appl
25	109	11.3	90	6	US-10-072-012-712		Sequence 712, App
26	109	11.3	90	6	US-10-072-012-713		Sequence 713, App

27	109	11.3	97	6	US-10-072-012-709	Sequence 709, App
28	109	11.3	97	6	US-10-072-012-711	Sequence 711, App
29	106	11.0	36	1	PCT-US02-31944A-34	Sequence 34, Appl
30	106	11.0	36	1	PCT-US02-30533A-34	Sequence 34, Appl
31	104.5	10.8	645	1	PCT-US02-40891-1630	Sequence 1630, Ap
32	104.5	10.8	645	1	PCT-US02-40892-617	Sequence 617, App
33	104	10.8	677	1	PCT-US02-40891-1675	Sequence 1675, Ap
34	104	10.8	677	1	PCT-US02-40892-631	Sequence 631, App
35	102	10.6	3014	1	PCT-US02-28859-107	Sequence 107, App
36	102	10.6	3014	6	US-10-241-220-107	Sequence 107, App
37	102	10.6	3014	6	US-10-225-567A-444	Sequence 444, App
38	102	10.6	3028	6	US-10-150-811-14	Sequence 14, Appl
39	102	10.6	3028	6	US-10-150-811-69	Sequence 69, Appl
40	102	10.6	3028	6	US-10-131-409-14	Sequence 14, Appl
41	102	10.6	3028	6	US-10-131-409-69	Sequence 69, Appl
42	102	10.6	3028	6	US-10-139-854-14	Sequence 14, Appl
43	102	10.6	3028	6	US-10-139-854-69	Sequence 69, Appl
44	102	10.6	3028	6	US-10-150-813-14	Sequence 14, Appl
45	102	10.6	3028	6	US-10-150-813-69	Sequence 69, Appl

ALIGNMENTS

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RESULT 1
PCT-US02-31944A-25
; Sequence 25, Application PC/TUS0231944A
; GENERAL INFORMATION:
; APPLICANT: Imperial College Innovations Limited
; APPLICANT: Bloom, Stephen R.
; APPLICANT: Small, Caroline J.
; APPLICANT: Batterham, Rachel L.
; APPLICANT: Ghatel, Mohammad A.
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Modification of Feeding Behavior
; FILE REFERENCE: 899-63727
; CURRENT APPLICATION NUMBER: PCT/US02/31944A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: GB 0200507.2
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 335
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Ovis aries
PCT-US02-31944A-25

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Query Match          19.3%; Score 186; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. NO. 3.8e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 30 APLEVPYPGDNATPEQMAQYAADLRRYINMLTRPR 64
Dd 1 APLEVPYPGDNATPEQMAQYAADLRRYINMLTRPR 35

RESULT 2
PCT-US02-30533A-25
; Sequence 25, Application PC/TUS0230533A
; GENERAL INFORMATION:
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Assessment of Neur

; FILE REFERENCE: 899-63986
; CURRENT APPLICATION NUMBER: PCT/US02/30533A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Bos taurus
PCT-US02-30533A-29

Query Match 18.3%; Score 176; DB 1; Length 36;
Best Local Similarity 94.3%; Pred. No. 2.1e-06;
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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|||||
Db 1 APLEPEYPGDNATPEQMAQYAAELRRYINMLTRPR 35

RESULT 11
PCT-US02-31944A-32
; Sequence 32, Application PC/TUS0231944A
; GENERAL INFORMATION:
; APPLICANT: Imperial College Innovations Limited
; APPLICANT: Bloom, Stephen R.
; APPLICANT: Small, Caroline J.
; APPLICANT: Batterham, Rachel L.
; APPLICANT: Ghatei, Mohammad A.
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Modification of Feeding Behavior
; FILE REFERENCE: 899-63727
; CURRENT APPLICATION NUMBER: PCT/US02/31944A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: GB 0200507.2
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 335
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Cavia porcellus
PCT-US02-31944A-32

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Best Local Similarity 91.7%; Pred. No. 6.3e-06;
Matches 33; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

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Db 1 APLEVPYPGDNATPEQMAQYAAEMRRYINMLTRPR 36

RESULT 12
PCT-US02-30533A-32
; Sequence 32, Application PC/TUS0230533A
; GENERAL INFORMATION:
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding Be

; FILE REFERENCE: 899-63986
; CURRENT APPLICATION NUMBER: PCT/US02/30533A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Cavia porcellus
PCT-US02-30533A-32

Query Match 17.6%; Score 169.5; DB 1; Length 37;
Best Local Similarity 91.7%; Pred. No. 6.3e-06;
Matches 33; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

Qy 30 APLEVPYPGDNATPEQMAQYAADLRRYINMLTRPR 64
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Db 1 APLEVPYPGDNATPEQMAQYAAEMRRYINMLTRPR 36

RESULT 13
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; Sequence 3, Application PC/TUS0231944A
; GENERAL INFORMATION:
; APPLICANT: Imperial College Innovations Limited
; APPLICANT: Bloom, Stephen R.
; APPLICANT: Small, Caroline J.
; APPLICANT: Batterham, Rachel L.
; APPLICANT: Ghatei, Mohammad A.
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Modification of Feeding Behavior
; FILE REFERENCE: 899-63727
; CURRENT APPLICATION NUMBER: PCT/US02/31944A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: GB 0200507.2
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 335
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-31944A-3

Query Match 17.4%; Score 168; DB 1; Length 36;
Best Local Similarity 91.4%; Pred. No. 8e-06;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 30 APLEVPYPGDNATPEQMAQYAADLRRYINMLTRPR 64
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Db 1 ASLEPEYPGDNATPEQMAQYAAELRRYINMLTRPR 35

RESULT 14
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; Sequence 3, Application PC/TUS0230533A
; GENERAL INFORMATION:
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding Be

; FILE REFERENCE: 899-63986
; CURRENT APPLICATION NUMBER: PCT/US02/30533A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-30533A-3

Query Match 17.4%; Score 168; DB 1; Length 36;
Best Local Similarity 91.4%; Pred. No. 8e-06;
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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; Sequence 31, Application PC/TUS0231944A
; GENERAL INFORMATION:
; APPLICANT: Imperial College Innovations Limited
; APPLICANT: Bloom, Stephen R.
; APPLICANT: Small, Caroline J.
; APPLICANT: Batterham, Rachel L.
; APPLICANT: Ghatei, Mohammad A.
; APPLICANT: Cowley, Michael
; APPLICANT: Cone, Roger
; APPLICANT: Low, Malcolm
; APPLICANT: Butler, Andrew
; TITLE OF INVENTION: Modification of Feeding Behavior
; FILE REFERENCE: 899-63727
; CURRENT APPLICATION NUMBER: PCT/US02/31944A
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/324,406
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: GB 0200507.2
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/392,109
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 335
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US02-31944A-31

Query Match 16.0%; Score 154; DB 1; Length 36;
Best Local Similarity 82.9%; Pred. No. 8.4e-05;
Matches 29; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
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Db 1 APLEPMYPGDYATPEQMAQYETQLRRYINTLTRPR 35

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model
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(without alignments)
168.945 Million cell updates/sec

Title: US-09-965-528-16
Perfect score: 964
Sequence: 1 MAAARLCLSLLLSTCVALL.....FSEWGSPHAAVPRELSPLDL 178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	103.5	10.7	97	3	US-09-054-393-1 Sequence 1, Appli
3	103.5	10.7	97	3	US-08-994-946A-6 Sequence 6, Appli
4	103.5	10.7	97	4	US-09-229-900-1 Sequence 1, Appli
5	103.5	10.7	97	4	US-09-291-994-6 Sequence 6, Appli
6	100.5	10.4	505	1	US-08-221-750A-5 Sequence 5, Appli
7	99	10.3	36	1	US-07-882-923-3 Sequence 3, Appli
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15	99	10.3	36	4	US-09-229-900-2 Sequence 2, Appli
16	99	10.3	36	4	US-09-181-941-4 Sequence 4, Appli
17	99	10.3	36	5	PCT-US95-14303-1 Sequence 1, Appli
18	99	10.3	36	5	PCT-US95-14303-2 Sequence 2, Appli
19	98.5	10.2	2205	1	US-08-093-453B-2 Sequence 2, Appli
20	98	10.2	36	1	US-08-329-151-9 Sequence 9, Appli
21	96.5	10.0	649	4	US-09-192-909-2 Sequence 2, Appli
22	96	10.0	36	4	US-09-181-941-2 Sequence 2, Appli
23	94	9.8	36	4	US-09-181-941-1 Sequence 1, Appli
24	91	9.4	684	1	US-08-555-669-12 Sequence 12, Appl
25	91	9.4	684	3	US-09-073-663-12 Sequence 12, Appl
26	89.5	9.3	3033	1	US-07-925-695-5 Sequence 5, Appli
27	89	9.2	36	1	US-07-882-923-2 Sequence 2, Appli

28	89	9.2	36	1	US-08-338-395-3	Sequence 3, Appli
29	89	9.2	36	1	US-08-329-151-24	Sequence 24, Appl
30	89	9.2	36	3	US-08-907-403A-1	Sequence 1, Appli
31	89	9.2	36	4	US-09-181-941-3	Sequence 3, Appli
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33	86	8.9	36	1	US-07-882-923-1	Sequence 1, Appli
34	86	8.9	36	1	US-08-264-030-1	Sequence 1, Appli
35	86	8.9	36	1	US-08-338-395-4	Sequence 4, Appli
36	86	8.9	36	3	US-08-907-403A-2	Sequence 2, Appli
37	86	8.9	36	4	US-09-181-941-5	Sequence 5, Appli
38	86	8.9	36	5	PCT-US95-14303-4	Sequence 4, Appli
39	85	8.8	36	1	US-07-776-272-18	Sequence 18, Appl
40	85	8.8	762	1	US-08-642-255-120	Sequence 120, App
41	85	8.8	762	1	US-08-397-633A-31	Sequence 31, Appl
42	85	8.8	1291	4	US-09-150-460B-10	Sequence 10, Appl
43	85	8.8	1291	4	US-09-220-641-5	Sequence 5, Appli
44	85	8.8	1964	4	US-09-467-997-1	Sequence 1, Appli
45	84	8.7	747	4	US-09-347-878-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-806-203-1
; Sequence 1, Application US/08806203
; Patent No. 5830434
; GENERAL INFORMATION:
; APPLICANT: TAYLOR, IAN L.
; APPLICANT: GETTYS, THOMAS
; TITLE OF INVENTION: METHODS OF TREATING NON-INSULIN
; TITLE OF INVENTION: DEPENDENT DIABETES MELLITUS WITH PANCREATIC POLYPEPTIDE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/806,203
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 19070.0028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-806-203-1

Query Match 19.3%; Score 186; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64

Db 1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35

REFERENCE/DOCKET NUMBER: BMR350/48000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)639-6585
TELEFAX: (202)639-6604
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-229-900-1

Query Match 10.7%; Score 103.5; DB 4; Length 97;
Best Local Similarity 39.1%; Pred. No. 0.0025;
Matches 25; Conservative 12; Mismatches 18; Indels 9; Gaps 2;

1 MAAARCLSLLLSTCVALLLQPLLGAQGAPEPVYPGDNATPEQMAQYAADLRRYINML 60
9 LSGLTALSLLV---CLGAL---AEAYPSKPDNPGEDAPAEQMARYYSALRHYINLI 59

QY 61 TRPR 64
60 TRQR 63

RESULT 5
US-09-291-994-6
Sequence 6, Application US/09291994
Patent No. 6312898
GENERAL INFORMATION:
APPLICANT: Koulu, Markku
APPLICANT: Karvonen, Matti
APPLICANT: Pesonen, Ullamari
APPLICANT: Uusitupa, Matti
TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing
TITLE OF INVENTION: Atherosclerosis or Diabetic Retinopathy Based on Leucine
TITLE OF INVENTION: 7 to Proline 7 Polymorphism in the Prepro-Neuropeptide
TITLE OF INVENTION: Y Gene.
FILE REFERENCE: 2328-112.A
CURRENT APPLICATION NUMBER: US/09/291,994
CURRENT FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 97
TYPE: PRT
ORGANISM: Homo sapiens
US-09-291-994-6

Query Match 10.7%; Score 103.5; DB 4; Length 97;
Best Local Similarity 39.1%; Pred. No. 0.0025;
Matches 25; Conservative 12; Mismatches 18; Indels 9; Gaps 2;

1 MAAARCLSLLLSTCVALLLQPLLGAQGAPEPVYPGDNATPEQMAQYAADLRRYINML 60
9 LSGLTALSLLV---CLGAL---AEAYPSKPDNPGEDAPAEQMARYYSALRHYINLI 59

QY 61 TRPR 64
60 TRQR 63

RESULT 6
US-08-221-750A-5
Sequence 5, Application US/08221750A
Patent No. 5643747
GENERAL INFORMATION:
APPLICANT: Baker, Steven M.
APPLICANT: Deich, Robert A.
TITLE OF INVENTION: Genes for the Export of Pertussis

TITLE OF INVENTION: Holotoxin
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,750A
FILING DATE: 31-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,619
FILING DATE: 15-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: ACC93-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-221-750A-5

Query Match 10.4%; Score 100.5; DB 1; Length 505;
Best Local Similarity 27.5%; Pred. No. 0.04;
Matches 55; Conservative 14; Mismatches 70; Indels 61; Gaps 11;

1 MAAARCLSLLLSTCVALLLQPLLGAQGAPEPVYPGDNATPEQMAQ--YAADLRRYI 57
333 MAAATLCAT---ATLMLTLVPLASSVNAGLRRRLWP--NAAHPGLAQAHRAAQA 386
58 NMLTRPCVQLGREIPAPGTGLPHIPGHTLSPAPAPAPSRPALGKTGHLCTGLDQCA 117
387 R-----RPAASAAAAGPHQAGTYAASATPAPAPAPSPAPSPFAH----AYQYA 430
118 L-GKMVPTG-----RYETGGLAPGHSACPCLFP-----PRYK 150
431 LGGARSPAGPGCDATTGPRRRRTDGFPP---ANPTCHDPRTFQRQIIAMGHPGHRPHAR 487

QY 151 RHKEDTLAFSEWGSPPHAAVP 170
488 RLR-----PEAGRPACRIP 501

RESULT 7
US-07-892-923-3
Sequence 3, Application US/07882923
Patent No. 5328899
GENERAL INFORMATION:
APPLICANT: Boublik, Jaroslav H.
APPLICANT: Rivier, Jean E.F.
APPLICANT: Brown, Marvin R.
APPLICANT: Scott, Neal A.
TITLE OF INVENTION: NPY PEPTIDE ANALOGS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 4250 Executive Square, Suite 510
CITY: La Jolla
STATE: CA

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; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/882,923
; FILING DATE: 19920512
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/503,198
; FILING DATE: 30-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/219,596
; FILING DATE: 15-JUL-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Schumann, James J.
; REGISTRATION NUMBER: 20,856
; REFERENCE/DOCKET NUMBER: 52864
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-552-1311
; TELEFAX: 619-552-0095
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-07-882-923-3

Query Match 10.3%; Score 99; DB 1; Length 36;
Best Local Similarity 47.1%; Pred. No. 0.002;
Matches 16; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
| : | | : : | | : : | | : : | | : : | |
Db 2 PAKPEAPGEDASPELSRYAYASLRHYLNLVTRQR 35

RESULT 8
US-08-338-395-1
; Sequence 1, Application US/08338395
; Patent No. 5574010
; GENERAL INFORMATION:
; APPLICANT: McFadden, David W
; TITLE OF INVENTION: TREATMENT OF PANCREATIC TUMORS WITH
; TITLE OF INVENTION: PEPTIDE YY AND ANALOGS THEREOF
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POMS, SMITH, LANDE & ROSE
; STREET: 2029 Century Park East 38th Floor
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,395
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J
; REGISTRATION NUMBER: 29421
; REFERENCE/DOCKET NUMBER: 107012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-788-5046
; TELEFAX: 310-277-1297
```

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: porcine peptide YY
US-08-338-395-1

Query Match 10.3%; Score 99; DB 1; Length 36;
Best Local Similarity 47.1%; Pred. No. 0.002;
Matches 16; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
| : | | : : | | : : | | : : | | : : | |
Db 2 PAKPEAPGEDASPELSRYAYASLRHYLNLVTRQR 35

RESULT 9
US-08-338-395-2
; Sequence 2, Application US/08338395
; Patent No. 5574010
; GENERAL INFORMATION:
; APPLICANT: McFadden, David W
; TITLE OF INVENTION: TREATMENT OF PANCREATIC TUMORS WITH
; TITLE OF INVENTION: PEPTIDE YY AND ANALOGS THEREOF
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POMS, SMITH, LANDE & ROSE
; STREET: 2029 Century Park East 38th Floor
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,395
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J
; REGISTRATION NUMBER: 29421
; REFERENCE/DOCKET NUMBER: 107012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-788-5046
; TELEFAX: 310-277-1297
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN PEPTIDE YY
US-08-338-395-2

Query Match 10.3%; Score 99; DB 1; Length 36;
Best Local Similarity 47.1%; Pred. No. 0.002;
Matches 16; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
| : | | : : | | : : | | : : | | : : | |
Db 2 PIKPEAPGEDASPEELNRYAYASLRHYLNLVTRQR 35

RESULT 10
US-08-329-151-1
; Sequence 1, Application US/08329151
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; Patent No. 5604203
; GENERAL INFORMATION:
; APPLICANT: Balasubramaniam, A.
; TITLE OF INVENTION: ANALOGS OF PEPTIDE YY AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,151
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/038,534
; FILING DATE: 3/29/93
; APPLICATION NUMBER: 08/109,326
; FILING DATE: 08/19/93
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00537/105001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: linear
; US-08-329-151-1

Query Match 10.3%; Score 99; DB 1; Length 36;
Best Local Similarity 47.1%; Pred. No. 0.002;
Matches 16; Conservative 11; Mismatches 7; Indels 0;

31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
|:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
2 PAKPEAPGEDASPELSRYAYASLRHYNLVTQR 35
```

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RESULT 11
US-08-329-151-2
; Sequence 2, Application US/08329151
; Patent No. 5604203
; GENERAL INFORMATION:
; APPLICANT: Balasubramaniam, A.
; TITLE OF INVENTION: ANALOGS OF PEPTIDE YY AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,151
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/038,534
; FILING DATE: 3/29/93
; APPLICATION NUMBER: 08/109,326
; FILING DATE: 08/19/93
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00537/105001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: linear
; US-08-329-151-2

Query Match 10.3%; Score 99; DB 1; Length 36;
Best Local Similarity 47.1%; Pred. No. 0.002;
Matches 16; Conservative 11; Mismatches 7; Indels 0;

QY 31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
|:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db 2 PIKPEAPGEDASPELNRYAYASLRHYNLVTQR 35

RESULT 12
US-09-054-393-2
; Sequence 2, Application US/09054393
; Patent No. 6017879
; GENERAL INFORMATION:
; APPLICANT: Mutter, Manfred
; APPLICANT: Lacroix, Jean S.
; APPLICANT: Grouzmann, Eric
; TITLE OF INVENTION: Template Associated NPY Y2-Receptor
; TITLE OF INVENTION: Agonists
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vinson & Elkins LLP
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20004-1008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,393
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanzo, Michael A.
; REGISTRATION NUMBER: 36,912
; REFERENCE/DOCKET NUMBER: BMR350/48000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)639-6585
; TELEFAX: (202)639-6604
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 1, 2003, 09:11:12 ; Search time 30 Seconds
(without alignments)
1222.546 Million cell updates/sec

Title: US-09-965-528-16
Perfect score: 964
Sequence: 1 MAAARLCUSLLLLSTCVALL.....FSEWGSPPHAAVPRELSPLDL 178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues 671580
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 21.*
- 1: sp_archea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	17.5	59	6 Q9GKL0	Q9gkl0 sus scrofa
2	115.5	12.0	95	13 Q9I9D3	Q9i9d3 ictalurus p
3	113.5	11.8	98	11 Q91XD0	Q91xd0 mus musculu
4	111	11.5	542	2 O68872	O68872 myxococcus
5	110.5	11.5	89	11 Q925V2	Q925v2 mus musculu
6	110.5	11.5	99	13 Q90WF4	Q90wf4 paralichthy
7	106	11.0	97	6 Q8SPF7	Q8spf7 ovis aries
8	105	10.9	97	6 Q9XSW6	Q9xsw6 macaca mula
9	105	10.9	99	13 Q90WF3	Q90wf3 paralichthy
10	104.5	10.8	90	6 Q9TSI6	Q9tsi6 ovis aries
11	104	10.8	97	13 Q9PW68	Q9pw68 typhlonecte
12	102.5	10.6	387	2 O52861	O52861 bacillus su
13	102	10.6	1334	16 Q9RKR9	Q9rkr9 streptomyce
14	102	10.6	3014	4 Q9NYQ6	Q9nyq6 homo sapien
15	101	10.5	96	13 Q9DGK7	Q9dgk7 cyprinus ca
16	97.5	10.1	387	16 O32062	O32062 bacillus su

17	96.5	10.0	2129	12 Q9J6K9	Q9j6k9 rubella vir
18	95.5	9.9	2115	12 Q86500	Q86500 rubella vir
19	95	9.9	36	6 Q9TR93	Q9tr93 oryctolagus
20	95	9.9	1203	4 Q9UMQ7	Q9umq7 homo sapien
21	95	9.9	1203	4 Q9Y3Q4	Q9y3q4 homo sapien
22	95	9.9	1838	5 Q960G3	Q960g3 drosophila
23	94.5	9.8	2116	12 Q99IE7	Q99ie7 rubella vir
24	94.5	9.8	2116	12 Q99IE5	Q99ie5 rubella vir
25	94.5	9.8	2116	12 Q8VAL1	Q8vall rubella vir
26	94	9.8	301	5 Q9XUT4	Q9xut4 caenorhabdi
27	94	9.8	545	4 Q9NX25	Q9nx25 homo sapien
28	94	9.8	1400	4 Q9NZ71	Q9nz71 homo sapien
29	94	9.8	1790	5 Q9VUH6	Q9vuh6 drosophila
30	93.5	9.7	572	3 Q9P4V1	Q9p4v1 candida boi
31	93.5	9.7	893	4 Q9Y2G1	Q9y2g1 homo sapien
32	93.5	9.7	1111	4 Q9P1Q6	Q9plq6 homo sapien
33	93.5	9.7	2116	12 Q8VAL3	Q8val3 rubella vir
34	93	9.6	702	11 Q9JME1	Q9jme1 mus musculu
35	93	9.6	774	16 Q9L0Z1	Q9l0z1 streptomyce
36	93	9.6	854	11 Q9QZS8	Q9qzs8 mus musculu
37	93	9.6	1161	4 Q9UPR4	Q9upr4 homo sapien
38	92.5	9.6	97	13 Q90WF2	Q90wf2 paralichthy
39	92.5	9.6	675	11 Q91YM9	Q91ym9 mus musculu
40	92.5	9.6	1123	11 Q9DBD5	Q9dbd5 mus musculu
41	92.5	9.6	1712	10 Q9AXN1	Q9axn1 botryoccladi
42	92.5	9.6	2116	12 O40955	O40955 rubella vir
43	92.5	9.6	2344	5 Q9N3Y8	Q9n3y8 caenorhabdi
44	91.5	9.5	577	10 Q9STP1	Q9stpl arabidopsis
45	91	9.4	295	5 Q20927	Q20927 caenorhabdi

ALIGNMENTS

RESULT 1

Q9GKL0 ID Q9GKL0 PRELIMINARY; PRT; 59 AA.
AC Q9GKL0;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Panceatic polypeptide (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Han X.G., Tuch B.E.;
RT "Partial porcine panceatic polypeptide cDNA sequence (3'end).";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
DR EMBL; AF203915; AAG35647.1; -.
DR HSSP; P01302; 1BBA.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
KW Amidation.
FT NON_TER 1
SQ SEQUENCE 59 AA; 6683 MW; 9A199783B9E29FCD CRC64;

Query Match 17.5%; Score 169; DB 6; Length 59;
Best Local Similarity 31.2%; Pred. No. 2.6e-08;
Matches 44; Conservative 5; Mismatches 8; Indels 84; Gaps 2;

Qy 36 YPGDNATPEQMAQYAADLRRYINMLTRPCVPCVQLGREIPAPGTLGPLHIPGHTLSPAPAP 95

Db 1 YPGDDATPEQMAQYAELRRYINMLTR----- 27

Qy 96 APSRPALGKTGHLCTGLDQCALGKMVPTGRYETGTGLAPGHSACPCCLFPFPRYCKRHKED 155


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KW Amidation.
SQ SEQUENCE 97 AA; 10840 MW; 2D2209BAC20BD5EE CRC64;

Query Match      10.9%; Score 105; DB 6; Length 97;
Best Local Similarity 40.6%; Pred. No. 0.027;
Matches 26; Conservative 13; Mismatches 23; Indels 2; Gaps 1;

QY 1 MAAARLCLSLLLSTCVALLLQPLLGAAQGAPLEVPVPGDNATPEQMAQYAADLRRYINML 60
   : : ||| | | | : : : : | : | : | : | : | : | : | : | : | : | : | :
Db 2 LGSKRLGLSLGLTALSLLVCLGAL--AEAYPSKPDNPGEDAPAEADMARYYSALRHYINLI 59

QY 61 TRPR 64
   || |
Db 60 TRQR 63

RESULT 9
Q90WF3 PRELIMINARY; PRT; 99 AA.
AC Q90WF3;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Peptide YY.
PY.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidei; Paralicthyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Kurokawa T., Suzuki T.;
RT "Development of neuropeptide Y related peptides in the digestive
RT organs during the larval stage of Japanese flounder, Paralicthys
RT olivaceus.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB055212; BAB62410.1; -.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR ProDom; PD001267; Pancreatic_hormn; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; UNKNOWN_1.
DR PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
SQ SEQUENCE 99 AA; 11179 MW; 32F6C21217CB1984 CRC64;

Query Match      10.9%; -Score 105; DB 13; Length 99;
Best Local Similarity 34.4%; Pred. No. 0.028;
Matches 22; Conservative 14; Mismatches 26; Indels 2; Gaps 1;

QY 1 MAAARLCLSLLLSTCVALLLQPLLGAAQGAPLEVPVPGDNATPEQMAQYAADLRRYINML 60
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1 MRSSTVMSPSVLALCLLACIHS--GINAYPVKPTIPREGATPEDLAKYYSALRHYINLI 58

QY 61 TRPR 64
   || |
Db 59 TRQR 62

RESULT 10
Q9TSI6 PRELIMINARY; PRT; 90 AA.
AC Q9TSI6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Neuropeptide Y (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RA Simmons J.M., Daniel J.A., Matteri R.L., Keisler D.H.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
DR EMBL; AF095782; AAC69886.1; -.
DR HSSP; P01303; IRON.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR PRINTS; PR00278; PANCHORMONE.
DR ProDom; PD001267; Pancreatic_hormn; 1.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
KW Amidation.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 9916 MW; 46FF2FB153EE5FFB CRC64;

Query Match      10.8%; Score 104.5; DB 6; Length 90;
Best Local Similarity 39.1%; Pred. No. 0.028;
Matches 25; Conservative 12; Mismatches 18; Indels 9; Gaps 2;

QY 1 MAAARLCLSLLLSTCVALLLQPLLGAAQGAPLEVPVPGDNATPEQMAQYAADLRRYINML 60
   : : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 4 LSLGLTALSLLV---CLGAL-----AEAYPSKPDNPGDDAPAEDELARYYSALRHYINLI 54

QY 61 TRPR 64
   || |
Db 55 TRQR 58

RESULT 11
Q9PW68 PRELIMINARY; PRT; 97 AA.
AC Q9PW68;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Neuropeptide Y precursor (NPY).
GN NPY.
OS Typhlonectes natans (Rio Cauca caecilian).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Gymnophiona; Caeciliidae; Typhlonectes.
OX NCBI_TaxID=8456;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 29-64, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=BRAIN;
RX MEDLINE=21184972; PubMed=11287086;
RA Ebersole T.J., Conlon J.M., Goetz F.W., Boyd S.K.;
RT "Characterization and distribution of neuropeptide Y in the brain of a
RT caecilian amphibian.";
RL Peptides 22:325-334(2001).
CC -!- FUNCTION: NPY IS IMPLICATED IN THE CONTROL OF FEEDING AND IN
CC SECRETION OF GONADOTROPHIN-RELEASE HORMONE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED THROUGHOUT THE BRAIN WITH HIGHEST
CC LEVELS OF EXPRESSION IN MEDIAL PALLIUM, BASAL FOREBRAIN, PREOPTIC
CC AREA, MIDBRAIN TEGMENTUM AND TRIGEMINAL NUCLEUS.
CC -!- MASS SPECTROMETRY: MW=4246; MW ERR=4; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
DR EMBL; AF167559; AAD48033.1; -.
DR HSSP; P01303; IRON.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR PRINTS; PR00278; PANCHORMONE.
DR ProDom; PD001267; Pancreatic_hormn; 1.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
KW Neuropeptide; Cleavage on pair of basic residues; Signal; Amidation.
FT SIGNAL 1 28
```


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OM protein - protein search, using sw model

Run On: March 1, 2003, 09:11:12 ; Search time 17 Seconds
(without alignments)
1006.584 Million cell updates/sec

Title: US-09-965-528-16
Perfect score: 964
Sequence: 1 MAAARLCLSLLLSTCVALL.....FSEWGSFHAAVPRELSPLDL 178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73.*
1: P1r1.*
2: P1r2.*
3: P1r3.*
4: P1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	441.5	45.8	95	1 PCHU	pancreatic hormone
2	305.5	31.7	93	1 PCDG	pancreatic hormone
3	260.5	27.0	100	2 B28261	pancreatic hormone
4	249.5	25.9	66	1 PCCT	pancreatic hormone
5	244.5	25.4	126	2 A28256	pancreatic hormone
6	236.5	24.5	98	1 PCRT	pancreatic hormone
7	207.5	21.5	59	1 PCSH	pancreatic hormone
8	186	19.3	36	2 C60071	pancreatic hormone
9	182	18.9	36	1 C61132	pancreatic hormone
10	180	18.7	36	1 A61132	pancreatic hormone
11	180	18.7	36	1 D61132	pancreatic hormone
12	180	18.7	36	2 B60413	pancreatic hormone
13	177	18.4	36	1 PCPG	pancreatic hormone
14	176	18.3	36	1 PCBO	pancreatic hormone
15	172	17.8	36	1 B61132	pancreatic hormone
16	161	16.7	36	2 JQ0365	pancreatic hormone
17	140	14.5	93	2 I50809	peptide YY - river
18	123	12.8	36	2 A28091	pancreatic hormone
19	116	12.0	98	2 A29364	peptide YY precurs
20	114	11.8	36	1 PCFG	pancreatic hormone
21	111.5	11.6	98	2 A25916	neuropeptide Y pre
22	110.5	11.5	97	2 JCI460	neuropeptide Y pre
23	110	11.4	80	1 PCCH	pancreatic hormone
24	109	11.3	90	2 S34569	peptide YY precurs
25	109	11.3	90	2 S34568	peptide YY precurs
26	109	11.3	97	2 S33795	peptide YY (clone
27	106	11.0	36	1 PCAQ	pancreatic hormone
28	103.5	10.7	97	1 NYHUY	neuropeptide Y pre
29	103	10.7	97	2 A41979	neuropeptide Y pre

30	102	10.6	104	2	I50808	neuropeptide Y pre
31	102	10.6	1334	2	T50568	probable multi-dom
32	101	10.5	37	2	S26954	peptide YY-related
33	100	10.4	96	2	B41979	neuropeptide Y pre
34	99	10.3	36	1	YYPG	peptide YY - pig
35	99	10.3	36	2	A31358	peptide YY - human
36	99	10.3	36	2	A60416	peptide YY - dog
37	98.5	10.2	2205	1	MNWRN	nonstructural poly
38	98	10.2	97	2	A55914	peptide YY precurs
39	97.5	10.1	387	2	H69971	spore coat protein
40	97.5	10.1	1042	1	CGCH1S	collagen alpha 1(I
41	97	10.1	1373	1	A43291	collagen alpha 2(I
42	96	10.0	36	1	PCGXA	pancreatic peptide
43	96	10.0	36	1	PCDFY	pancreatic peptide
44	96	10.0	36	2	A49743	pancreatic peptide
45	95.5	9.9	2115	2	S38480	nonstructural prot

ALIGNMENTS

RESULT 1

PCHU

pancreatic hormone precursor [validated] - human
N;Alternate names: pancreatic polypeptide precursor
N;Contains: pancreatic heptapeptide; pancreatic icosapeptide
C;Species: Homo sapiens (man)

C;Date: 17-Dec-1982 #sequence_revision 25-Feb-1985 #text_change 08-Dec-2000
C;Accession: A92498; A91002; A22587; I70196; A94026; A94018; A60068; A01566
R;Leiter, A.B.; Montminy, M.R.; Jamieson, E.; Goodman, R.H.

J. Biol. Chem. 260, 13013-13017, 1985
A;Title: Exons of the human pancreatic polypeptide gene, define functional domains of the
A;Reference number: A92498; MUID:86033734; PMID:2997153
A;Accession: A92498

A;Molecule type: DNA
A;Residues: 1-95 <LEI1>

A;Cross-references: GB:M11726; NID:gl90269; PIDN:AAA60156.1; PID:gl90270
R;Boel, E.; Schwartz, T.W.; Norris, K.E.; Fill, N.P.
EMBO J. 3, 909-912, 1984

A;Title: A cDNA encoding a small common precursor for human pancreatic polypeptide and I
A;Reference number: A91002; MUID:84207951; PMID:6373251
A;Accession: A91002

A;Molecule type: mRNA
A;Residues: 1-95 <BOE>

A;Cross-references: GB:X00491; NID:g35589; PIDN:CAA25161.1; PID:g35590
R;Leiter, A.B.; Keutmann, H.T.; Goodman, R.H.
J. Biol. Chem. 259, 14702-14705, 1984

A;Title: Structure of a precursor to human pancreatic polypeptide.
A;Reference number: A22587; MUID:85054955; PMID:6094571

A;Accession: A22587

A;Molecule type: mRNA

A;Residues: 1-95 <LEI2>

A;Note: part of this sequence, including the amino end of the mature protein, was deter
R;Takeuchi, T.; Gumucio, D.L.; Yamada, T.; Meisler, M.H.; Minth, C.D.; Dixon, J.E.; Edd
J. Clin. Invest. 77, 1038-1041, 1986

A;Title: Genes encoding pancreatic polypeptide and neuropeptide Y are on human chromosom
A;Reference number: I55543; MUID:86140715; PMID:3753985

A;Accession: I70196

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-85, 'I', 87-95 <TAK1>

A;Cross-references: GB:M15788; NID:gl90301; PIDN:AAA60161.1; PID:gl90302

R;Takeuchi, T.; Yamada, T.

Proc. Natl. Acad. Sci. U.S.A. 82, 1536-1539, 1985

A;Title: Isolation of a cDNA clone encoding pancreatic polypeptide.

A;Reference number: A94026; MUID:85140331; PMID:3856278

A;Accession: A94026

A;Molecule type: mRNA

A;Residues: 1-85, 'I', 87-95 <TAK2>

R;Schwartz, T.W.; Hansen, H.F.; Hakanson, R.; Sundler, F.; Tager, H.S.

Proc. Natl. Acad. Sci. U.S.A. 81, 708-712, 1984

A;Title: Human pancreatic icosapeptide: isolation, sequence, and immunocytochemical loca

A;Reference number: A94018; MUID:84144773; PMID:6366786

A;Accession: A94018
A;Molecule type: protein
A;Residues: 69-88 <SCH>
R;Gingerich, R.L.; Akpan, J.O.; Leith, K.M.; Gilbert, W.R.
Regul. Pept. 33, 275-285, 1991
A;Title: Patterns of immunoreactive pancreatic polypeptide in human plasma.
A;Reference number: A60068; MUID:91352354; PMID:1882090
A;Accession: A60068
A;Molecule type: protein
A;Residues: 32-47 <GIN>
C;Genetics:
A;Gene: GDB:PPY
A;Cross-references: GDB:120311; OMIM:167780
A;Map position: 17q12-17q21
A;Introns: 64/2; 88/2
C;Superfamily: pancreatic hormone
C;Keywords: amidated carboxyl end; hormone; pancreas
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-65/Product: pancreatic hormone #status predicted <PCH>
F;69-88/Product: pancreatic icosapeptide #status experimental <PCI>
F;89-95/Product: pancreatic heptapeptide #status predicted <PC7>
F;65/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly

Query Match 45.8%; Score 441.5; DB 1; Length 95;
Best Local Similarity 53.4%; Pred. No. 7e-28;
Matches 95; Conservative 0; Mismatches 0; Indels 83; Gaps 1;

QY 1 MAAARLCLSLLLSTCVALLLQPLLGAQGAPLEVPYPGDNATPEQMAQYAADLRRYINML 60
|||
Db 1 MAAARLCLSLLLSTCVALLLQPLLGAQGAPLEVPYPGDNATPEQMAQYAADLRRYINML 60
|||

QY 61 TRPRCVPQLGREIPAPGTGLPLHIPGHTLSAPAPAPSRPALGKTGHLCTGLDQCALGK 120
||
Db 61 TR----- 62

QY 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPPHAAVPREL 178
|||
Db 63 -----PRYGKRHKEDTLAFSEWGSPPHAAVPRELSPDL 95

RESULT 2
PCDG
pancreatic hormone precursor - dog
N;Alternate names: pancreatic polypeptide precursor
N;Contains: pancreatic hormone; pancreatic icosapeptide
C;Species: Canis lupus familiaris (dog)
C;Date: 25-Feb-1985 #sequence revision 12-Apr-1996 #text_change 18-Jun-1999
C;Accession: A40904; A94465; A93270; A01567
R;Toothman, P.; Paquette, T.L.
Endocrinol. 1, 413-419, 1987
A;Title: Canine pancreatic polypeptide complementary deoxyribonucleic acid sequence: pan
A;Reference number: A40904; MUID:90331935; PMID:3079195
A;Accession: A40904
A;Molecule type: mRNA
A;Residues: 1-93 <TOO>
A;Cross-references: GB:M35596; NID:g164049; PIDN:AAA30886.1; PID:g164050
A;Note: the authors translated the codon CCT for residue 2 as Ala, and GAG for residue 5
R;Chance, R.E.; Johnson, M.G.; Hoffmann, J.A.; Jones, W.E.; Koffenberger Jr., J.E.
unpublished results, cited by Chance, R.E., Moon, N.E., and Johnson, M.G., in Methods of
San Francisco, and London, 1979
A;Reference number: A94465
A;Accession: A94465
A;Molecule type: protein
A;Residues: 30-65 <CHA>
R;Schwartz, T.W.; Tager, H.S.
Nature 294, 589-591, 1981
A;Title: Isolation and biogenesis of a new peptide from pancreatic islets.
A;Reference number: A93270; MUID:82080694; PMID:7031480
A;Accession: A93270
A;Molecule type: protein
A;Residues: 69-88 <SCH>
C;Comment: The hormone precursor molecules are stored in islet cells of the duodenal pan
C;Superfamily: pancreatic hormone

C;Keywords: amidated carboxyl end; hormone; pancreas
F;1-20/Domain: signal sequence #status predicted <SIG>
F;30-65/Product: pancreatic hormone #status experimental <PCH>
F;69-88/Product: pancreatic icosapeptide #status experimental <PCI>
F;65/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gl

Query Match 31.7%; Score 305.5; DB 1; Length 93;
Best Local Similarity 40.5%; Pred. No. 2.8e-17;
Matches 70; Conservative 5; Mismatches 15; Indels 83; Gaps 1;

QY 1 MAAARLCLSLLLSTCVALLLQPLLGAQGAPLEVPYPGDNATPEQMAQYAADLRRYINML 60
|||
Db 1 MPAACRCLFLLLSACVALLLQPLGTRGAPLEVPYPGDDATPEQMAQYAAELRRYINML 60
|||

QY 61 TRPRCVPQLGREIPAPGTGLPLHIPGHTLSAPAPAPSRPALGKTGHLCTGLDQCALGK 120
||
Db 61 TR----- 62

QY 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPPHAAVPREL 173
|||
Db 63 -----PRYGKRDRGEMRDILEWGSPPHAAAPREL 90

RESULT 3
B28261
pancreatic hormone precursor - mouse
N;Alternate names: pancreatic polypeptide precursor
N;Contains: pancreatic hormone; pancreatic icosapeptide
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: B28261
R;Yonekura, H.; Nata, K.; Watanabe, T.; Kurashina, Y.; Yamamoto, H.; Okamoto, H.
J. Biol. Chem. 263, 2990-2997, 1988
A;Title: Mosaic evolution of prepropancreatic polypeptide. Structural conservation and
A;Reference number: A92708; MUID:88139354; PMID:3343236
A;Accession: B28261
A;Molecule type: DNA
A;Residues: 1-100 <YON>
A;Cross-references: GB:M18208; GB:J03543; NID:g200463; PIDN:AAA39967.1; PID:g200464
C;Superfamily: pancreatic hormone
C;Keywords: amidated carboxyl end; hormone; pancreas
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-65/Product: pancreatic hormone #status predicted <PCH>
F;71-100/Product: pancreatic icosapeptide #status predicted <PCI>
F;65/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gl

Query Match 27.0%; Score 260.5; DB 2; Length 100;
Best Local Similarity 61.1%; Pred. No. 9.7e-14;
Matches 58; Conservative 5; Mismatches 25; Indels 7; Gaps 2;

QY 1 MAAARLCLSLLLSTCVALLLQPLLGAQGAPLEVPYPGDNATPEQMAQYAADLRRYINML 60
|||
Db 1 MAVAYCCLSLFLVSTVALLLQPLQGTWGAPLEPMYPYPGDYATPEQMAQYETQLRRYINTL 60
|||

QY 61 TRPRCVPQLGREIPAPGTGLPLHIPGHTLSAPAP 95
|||
Db 61 TRPR----YGKRAEENTGG--LPGVQLSPCTSP 88
|||

RESULT 4
PCCT
pancreatic hormone precursor - cat (tentative sequence) (fragment)
N;Alternate names: pancreatic polypeptide precursor
N;Contains: pancreatic hormone; pancreatic icosapeptide
C;Species: Felis silvestris catus (domestic cat)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A26073
R;Nielsen, H.V.; Gether, U.; Schwartz, T.W.
Biochem. J. 240, 69-74, 1986
A;Title: Cat pancreatic icosapeptide and its biosynthetic intermediate. Conservation c
A;Reference number: A26073; MUID:87156600; PMID:3827854
A;Accession: A26073
A;Molecule type: protein

A;Molecule type: protein
A;Residues: 1-36 <ENG>
C;Superfamily: pancreatic hormone

Query Match	18.7%	Score 180;	DB 2;	Length 36;
Best Local Similarity	94.1%	Pred. NO. 6.9e-08;		
Matches 33;	Conservative	2;	Mismatches 0;	Indels 0;
			Gaps	0;

Qy 30 APLEVPYPGDNATPEQMAQYAADLRRYINMLTRPR 64
|||
Db 1 APLEVPYPGDNATPEQMAQYAAEMRRYINMLTRPR 35

RESULT 13
PCPG
pancreatic hormone - pig
N;Alternate names: pancreatic polypeptide
C;Species: Sus scrofa domestica (domestic pig)
Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 23-Aug-1996
Accession: A01568

A;Reference number: A01568
A;Accession: A01568
A;Molecule type: protein
A;Residues: 1-36 <CHA>
C;Superfamily: pancreatic hormone
F;Keywords: amidated carboxyl end; hormone; pancreas
F;1-36/Product: pancreatic hormone #status experimental <PCH>
F;36/Modified site: amidated carboxyl end (Tyr) #status experimental

```

Query Match      18.4%; Score 177; DB 1; Length 36;
Best Local Similarity 94.3%; Pred. No. 1.2e-07;
Matches 33: Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

Qy 30 APLEVPYPGDNATPEQMAQYAADLRRYYINMLTRPR 64
|||
|||
Db 1 APLEVPYPGDDATPEQMAQYAALRRYYINMLTRPR 35
|||
|||

RESULT 14
PCBO
pancreatic hormone - bovine
N;Alternate names: pancreatic polypeptide
C;Species: Bos primigenius taurus (cattle)
C;Date: 17-Dec-1982 #sequence revision17-Dec-1982 #text change 10-May-2001

Accession: A01570
Chance, R.E.; Johnson, M.G.; Hoffmann, J.A.; Jones, W.E.; Koffenberger Jr., J.E.
Published results, cited by Chance, R.E., Moon, N.E., and Johnson, M.G., in Methods of
San Francisco and London. 1979

A;Reference number: A94465
A;Accession: A01570
A;Molecule type: protein
A;Residues: 1-36 <CHA>
C;Superfamily: pancreatic hormone
C;Keywords: amidated carboxyl end; hormone; pancreas
F;1-36/Product: pancreatic hormone #status experimental <PCH>
F;36/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match	18.3%	Score 176;	DB 1;	Length 36;
Best Local Similarity	94.3%	Pred. No. 1.4e-07;		
Matches 33: Conservative	1: Mismatches	1: Indels	0: Gaps	0:

```

QY 30 APLEVPYPGDNATPEQMAQYAADLRRYINMLTPR 64
      |||||
db  1 APLEPEYPGDNATPEQMAQYAAELRRYINMLTPR 35

```

RESULT 15
B61132
pancreatic hormone - white rhinoceros
N;Alternate names: pancreatic polypeptide
C;Species: Ceratotherium simum (white rhinoceros, square-lipped rhinoceros)

C;Date: 10-Mar-1994 #sequence_revision 07-Oct-1994 #text_change 26-Feb-1999
C;Accession: B61132
R;Henry, J.S.; Lance, V.A.; Conlon, J.M.
Gen. Comp. Endocrinol. 84, 440-446, 1991
A;Title: Primary structure of pancreatic polypeptide from four species of p
A;Reference number: A61132; MUID:92225314; PMID:1808025

Query Match 17.8%; Score 172; DB 1; Length 36;
Best Local Similarity 91.4%; Pred. No. 2.9e-07;
Matches 32: Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 30 APLEVPYPGDNATPEQMAQYAADLRRYYINMLTRPR 64
:
pb 1 SPLEVPYPGDNATPELMAYAAELRRYYINMLTRPR 35

Search completed: March 1, 2003, 09:11:38
Job time : 18 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 1, 2003, 09:11:12 ; Search time 12 Seconds
(without alignments)
615.232 Million cell updates/sec

Title: US-09-965-528-16
Perfect score: 964
Sequence: 1 MAAARLCLSLLLSTCVALL.....FSEWSPHAAVPRELSPLDL 178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Aligned: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	441.5	45.8	95	1 PAHO_HUMAN	P01298 homo sapien
2	349.5	36.3	131	1 PAHO_BOVIN	P01302 bos taurus
3	305.5	31.7	93	1 PAHO_CANEA	P01299 canis famil
4	260.5	27.0	100	1 PAHO_MOUSE	P10601 mus musculu
5	249.5	25.9	66	1 PAHO_FELCA	P06884 felis silve
6	244.5	25.4	126	1 PAHO_CAVPO	P13083 cavia porce
7	236.5	24.5	98	1 PAHO_RAT	P06303 rattus norv
8	207.5	21.5	59	1 PAHO_SHEEP	P01301 ovis aries
9	186	19.3	36	1 PAHO_MACMU	P33684 macaca mula
10	182	18.9	36	1 PAHO_TAPPI	P39659 tapirus pin
11	180	18.7	36	1 PAHO_CHIBR	P41519 chinchilla
12	180	18.7	36	1 PAHO_EQUZE	P38000 equus zebra
13	177	18.4	36	1 PAHO_PIG	P01300 sus scrofa
14	176	18.3	36	1 PAHO_CERSI	P37999 ceratotheri
15	173	17.9	36	1 PAHO_ERIEU	P41335 erinaceus e
16	167	17.3	36	1 PAHO_RABIT	P41336 oryctolagus
17	161	16.7	36	1 PAHO_DIDMA	P18107 didelphis m
18	140	14.5	93	1 PYI_LAMFL	P48098 lampetra fl
19	123	12.8	36	1 PAHO_RANCA	P15427 rana catesb
20	116	12.0	98	1 PYI_RAT	P10631 rattus norv
21	115.5	12.0	95	1 NEUY_ICTPU	Q919d3 ictalurus p
22	114	11.8	36	1 PAHO_RANTE	P31229 rana tempor
23	113.5	11.8	93	1 PYI_MOUSE	Q9eps2 mus musculu
24	111.5	11.6	97	1 NEUY_MOUSE	P57774 mus musculu
25	111.5	11.6	98	1 NEUY_RAT	P07808 rattus norv
26	110.5	11.5	97	1 NEUY_XENLA	P33689 xenopus lae
27	110	11.4	80	1 PAHO_CHICK	P01306 gallus gall
28	109	11.3	97	1 PYI_HUMAN	P10082 homo sapien
29	108	11.2	97	1 PYI_BRARE	Q9i8p2 brachydanio
30	107	11.1	97	1 PYI_DICLA	Q9pt98 dicentrarch
31	106	11.0	36	1 PAHO_ALIMI	P06305 alligator m
32	106	11.0	99	1 PYI_DICLA	Q9pt99 dicentrarch
33	104.5	10.8	96	1 NEUY_BRARE	Q9i8p3 brachydanio

34	103.5	10.7	97	1 NEUY_HUMAN	P01303 homo sapien
35	103	10.7	97	1 NEUY_CHICK	P28673 gallus gall
36	102.5	10.6	99	1 NEUY_DICLA	Q9pta0 dicentrarch
37	102	10.6	104	1 NEUY_LAMFL	P48097 lampetra fl
38	102	10.6	3014	1 CLR1_HUMAN	Q9nyq6 homo sapien
39	101	10.5	36	1 PYI_RAJRH	P29206 raja rhina
40	101	10.5	37	1 PYI_CHICK	P29203 gallus gall
41	100	10.4	96	1 NEUY_CARAU	P28672 carassius a
42	99	10.3	36	1 PYI_PIG	P01305 sus scrofa
43	98.5	10.2	2205	1 POLN_RUBVT	P13889 rubella vir
44	98	10.2	97	1 PYI_BOVIN	P51694 bos taurus
45	97.5	10.1	1453	1 CALI_CHICK	P02457 gallus gall

ALIGNMENTS

RESULT 1
PAHO_HUMAN
ID PAHO_HUMAN STANDARD; PRT; 95 AA.
AC P01298;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pancreatic hormone precursor (Pancreatic polypeptide) (PP).
GN PPY OR PNP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84207951; PubMed=6373251;
RA Boel E., Schwartz T.W., Norris K.E., Fill N.P.;
RT "A cDNA encoding a small common precursor for human pancreatic
polypeptide and pancreatic icosapeptide.";
RL EMBO J. 3:909-912(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86033734; PubMed=2997153;
RA Leiter A.B., Montminy M.R., Jamieson E., Goodman R.H.;
RT "Exons of the human pancreatic polypeptide gene define functional
domains of the precursor.";
RL J. Biol. Chem. 260:13013-13017(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=85054955; PubMed=6094571;
RA Leiter A.B., Keutmann H.T., Goodman R.H.;
RT "Structure of a precursor to human pancreatic polypeptide.";
RL J. Biol. Chem. 259:14702-14705(1984).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=86140715; PubMed=37539985;
RA Takeuchi T., Gumucio D.L., Yamada T., Meisler M.H., Minth C.D.,
Dixon J.E., Eddy R.E., Shows T.B.;
RT "Genes encoding pancreatic polypeptide and neuropeptide Y are on
human chromosomes 17 and 7.";
RL J. Clin. Invest. 77:1038-1041(1986).
RN [5]
RP SEQUENCE OF 69-88.
RX MEDLINE=84144773; PubMed=6366786;
RA Schwartz T.W., Hansen H.F., Haakanson R., Sundler F., Tager H.S.;
RT "Human pancreatic icosapeptide: isolation, sequence, and
immunocytochemical localization of the COOH-terminal fragment of the
pancreatic polypeptide precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:708-712(1984).
CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
GASTROINTESTINAL FUNCTIONS.
CC -!- FUNCTION: THE PHYSIOLOGICAL ROLE FOR THE ICOSAPEPTIDE HAS
NOT YET BEEN ELUCIDATED.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYI FAMILY.

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DR EMBL; X00491; CAA25161.1; -;
DR EMBL; M11726; AAA60156.1; -;
DR EMBL; M15788; AAA60161.1; -;
DR PIR; A01566; PCHU.
DR PIR; A22587; A22587.
DR HSSP; P01302; LBBA.
DR Genew; HGNC:9327; PPY.
DR MIM; 167780; -;
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR PRINTS; PR00278; PANCHORMONE.
DR SMART; SM00309; PAH; 1.

PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
PROSITE; PS00276; PANCREATIC_HORMONE_2; 1.

KW Hormone; Cleavage on pair of basic residues; Pancreas; Signal;

KW Amidation.

FT SIGNAL 1 29

FT PEPTIDE 30 65 PANCREATIC_HORMONE.

FT PEPTIDE 69 88 PANCREATIC_ICOSAPEPTIDE.

FT PROPEP 89 95

FT MOD_RES 65 65

FT CONFLICT 86 86

SQ SEQUENCE 95 AA; 10445 MW; 44F0265092F9C4A0 CRC64;

Query Match 45.8%; Score 441.5; DB 1; Length 95;
Best Local Similarity 53.4%; Pred. No. 2e-27;
Matches 95; Conservative 0; Mismatches 0; Indels 83; Gaps 1;

QY 1 MAAARCLSLLLSTCVALLQPLLGAQAPLEVPYPGDNATPEQMAQYAADLRRYINML 60

|||||
1 MAAARCLSLLLSTCVALLQPLLGAQAPLEVPYPGDNATPEQMAQYAADLRRYINML 60

QY 61 TRPRCVPLGREIPAPGTGLPGLHPTLSPAPAPAPSRPALGKTGHLCTGLDQCALGK 120

|||

61 TR-----

QY 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPPHAAVRELSPDL 178

|||||

63 -----PRYGKRHKEDTLAFSEWGSPPHAAVRELSPDL 95

RESULT 2

PAHO BOVIN

ID PAHO BOVIN STANDARD; PRT; 131 AA.

AC P01302;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pancreatic hormone precursor (Pancreatic polypeptide) (PP).

GN PPY.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95132645; PubMed=7831336;

RA Herzog H., Hort Y., Schneider R., Shine J.;

RT "Seminaplasmin: recent evolution of another member of the

RT neuropeptide Y gene family.";

RL Proc. Natl. Acad. Sci. U.S.A. 92:594-598(1995).

RN [2]

RP SEQUENCE OF 30-65.

RA Chance R.E., Johnson M.G., Hoffmann J.A., Jones W.E.,
RA Koffenberger J.E. Jr.;
RL Unpublished results, cited by:
RL Chance R.E., Moon N.E., Johnson M.G.;
RL (In) Jaffe B.M., Behrman H.R. (eds.);
RL Methods of hormone radioimmunoassay (2nd ed.), pp.657-672,
RL Academic Press, New York and London (1979).
RN [3]

RP STRUCTURE BY NMR.

RX MEDLINE=92135211; PubMed=1734969;

RA Li X., Sutcliffe M.J., Schwartz T.W., Dodson C.M.;

RT "Sequence-specific 1H NMR assignments and solution structure of

RT bovine pancreatic polypeptide.";

RL Biochemistry 31:1245-1253(1992).

CC -!- FUNCTION: PANCREATIC_HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS

CC OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND

CC GASTROINTESTINAL FUNCTIONS.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PPY FAMILY.

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CC or send an email to license@isb-sib.ch).

DR EMBL; L33970; AAA98526.1; -;

DR PIR; A01570; PCBO.

DR PDB; 1BBA; 31-OCT-93.

DR InterPro; IPR001955; Pancreatic_hormn.

DR Pfam; PF00159; hormone3; 1.

DR PRINTS; PR00278; PANCHORMONE.

DR SMART; SM00309; PAH; 1.

DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.

DR PROSITE; PS00276; PANCREATIC_HORMONE_2; 1.

KW Hormone; Cleavage on pair of basic residues; Pancreas; Signal;

KW Amidation; 3D-structure.

FT SIGNAL 1 29

FT PEPTIDE 30 65 PANCREATIC_HORMONE.

FT PEPTIDE 69 89 C-TERMINAL PEPTIDE 1 (POTENTIAL).

FT PEPTIDE 93 131 C-TERMINAL PEPTIDE 2 (POTENTIAL).

FT MOD_RES 65 65 AMIDATION (G-66 PROVIDE AMIDE GROUP).

FT TURN 43 44

FT HELIX 45 60

SQ SEQUENCE 131 AA; 14375 MW; DCDPE1011C67DF9B CRC64;

Query Match 36.3%; Score 349.5; DB 1; Length 131;
Best Local Similarity 48.5%; Pred. No. 2.7e-20;
Matches 83; Conservative 3; Mismatches 26; Indels 59; Gaps 2;

QY 1 MAAARCLSLLLSTCVALLQPLLGAQAPLEVPYPGDNATPEQMAQYAADLRRYINML 60

|||||

1 MAAARCLFLLLSTCVALLQPLLGAQAPLEVPYPGDNATPEQMAQYAAELRRYINML 60

QY 61 TRPRCVPLGREIPAPGTGLPGLHPTLSPAPAPAPSRPALGKTGHLCTGLDQCALGK 120

|||||

61 TRPR-----YGK 67

QY 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPPHAAVPR 171

|||||

68 RDKEGTLDFLECGSPHSAV-----PRYGKRDKEGTLDFLECGSPHSVPR 112

RESULT 3

PAHO CANFA

ID PAHO CANFA STANDARD; PRT; 93 AA.

AC P01299;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pancreatic hormone precursor (Pancreatic polypeptide) (PP).


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DR HSSP; P01302; 1BBA.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR PRINTS; PR00278; PANCHORMONE.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS0276; PANCREATIC_HORMONE_2; 1.
DR Hormone; Amidation; Pancreas.
KW MOD_RES 36
SQ SEQUENCE 36 AA; 4198 MW; 7611D1DC71A6308F CRC64;

Query Match      18.4%; Score 177; DB 1; Length 36;
Best Local Similarity 94.3%; Pred. No. 1e-07;
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
Db 1 APLEPVYPGDDATPEQMAQYAELRRYINMLTRPR 35
      |||||:|||||:|||||:|||||:|||||
RESULT 14
PAHO_CERSI
ID PAHO_CERSI STANDARD; PRT; 36 AA.
AC P37939;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pancreatic hormone (Pancreatic polypeptide) (PP).
GN PPY.
OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX NCBI_TaxID=9807;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=92225314; PubMed=1808025;
RA Henry J.S., Lance V.A., Conlon J.M.;
RT "Primary structure of pancreatic polypeptide from four species of
RT Perissodactyla (Przewalski's horse, zebra, rhino, tapir).";
RL Gen. Comp. Endocrinol. 84:440-446(1991).
CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
CC OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
CC GASTROINTESTINAL FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
DR PIR; B61132; B61132.
DR HSSP; P01302; 1BBA.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR PRINTS; PR00278; PANCHORMONE.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS0276; PANCREATIC_HORMONE_2; 1.
DR Hormone; Amidation; Pancreas.
KW MOD_RES 36
SQ SEQUENCE 36 AA; 4214 MW; 761B716F8CE2908F CRC64;

Query Match      18.3%; Score 176; DB 1; Length 36;
Best Local Similarity 91.4%; Pred. No. 1.2e-07;
Matches 32; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
Db 1 SPLEPVYPGDDATPEQMAQYAELRRYINMLTRPR 35
      :|||||:|||||:|||||:|||||:|||||
RESULT 15
PAHO_ERIEU
ID PAHO_ERIEU STANDARD; PRT; 36 AA.
AC P41335;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pancreatic hormone (Pancreatic polypeptide) (PP).
GN PPY.
OS Erinaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.
OX NCBI_TaxID=9365;
RN (1)
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=94052825; PubMed=8234904;
RA Marks N.J., Shaw C., Halton D.W., Thim L.;
RT "The primary structure of pancreatic polypeptide from a primitive
insectivorous mammal, the European hedgehog (Erinaceus europaeus).";
RL Regul. Pept. 47:179-185(1993).
CC -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
GASTROINTESTINAL FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
HSSP; P01302; 1BBA.
InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3; 1.
DR PRINTS; PR00278; PANCHORMONE.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS00276; PANCREATIC_HORMONE_2; 1.
KW Hormone; Amidation; Pancreas.
FT MOD_RES 36 36 AMIDATION.
SQ SEQUENCE 36 AA; 4234 MW; 7609C6989148208F CRC64;

Query Match 17.9%; Score 173; DB 1; Length 36;
Best Local Similarity 94.1%; Pred. No. 2.1e-07;
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
|||
Db 2 PLEPVYPGDNATPEQMAHYAAELRRYINMLTRPR 35

Search completed: March 1, 2003, 09:11:58
Job time : 13 secs